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Perfect score:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

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     GenCore version 5.1.7
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Sequence 501, App
Sequence 10, Appli
Sequence 10, Appli
Sequence 118, App
Sequence 218, Appli
Sequence 218, Appli
Sequence 11, Appli
Sequence 631, Appli
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Similarity 100.0%; Score 1; Conservative 0; Mis METNETPLNEYSEVSYSSAGYTVLR METNESTPLNEYSEVSYSSAGYTVLR TICYLNLALADESETATLEFLIVSMA	plication 10120119494 ATION: Harion: Hehringer I NTION: Met NTION: in NTION:	00000000000000000000000000000000000000
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100.0%; Score 1817; DB 3; Length 3 100.0%; Pred. NO. 2.9e.148; EYESYSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIW EYESYSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIW EYESYSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIW EYESYSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIW DFSFTATLPFLIVSNAMGEKWPFGWFLCKLIHIVVDINL	KG ying substances ' atory conditions ay diseases 807	110-026-937-2 -10-251-385-246 -10-505-486-119 -10-026-102-4 -10-226-102-4 -10-226-102-17 -10-226-102-17 -10-225-385-270 -10-225-385-270 -10-225-385-270 -10-6407-079-17 -10-684-206-4 -10-017-161-760 -09-892-206-2 -10-046-857-4 -10-075-255A-4 -10-017-161-761 -10-046-857-4 -10-017-161-761
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Sequence 120, Application US/10225;
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph C.
APPLICANT: Roush, Christine L.
APPLICANT: Roush, Christine L.
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US-10-225-567A-120
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                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/10874015 Publication No. US20040253630A1 GENERAL INFORMATION:
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FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILLING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
SEQ ID NO 120
LENGTH: 351
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APPLICANT: Mueller, Stefan
APPLICANT: Kistler, Barbara
APPLICANT: Seither, Peter
APPLICANT: Gust, Karsten
APPLICANT: Weith, Andreas
TITLE OF INVENTION: Method for identifying substances which positively
TITLE OF INVENTION: influence inflammatory conditions of chronic
TITLE OF INVENTION: inflammatory airway diseases
FILE REFERENCE: 1/1144-1-D1
CURRENT APPLICATION NUMBER: US/10/874,015
CURRENT FILING DATE: 2004-06-22
PRIOR APPLICATION NUMBER: UK 0021484.1
PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                   APPLICANT: Jung, Birgit
APPLICANT: Kraut, Norbert
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ITITLE OF INVENTION: Oncology drug innovation

PILE REFERENCE: P 573 PC00

CURRENT APPLICATION NUMBER: US/10/482,029

CURRENT FILING DATE: 2003-12-29

NUMBER OF SEQ ID NOS: 437

SOFTWARE: PatentIn version 3.1

SEQ ID NO 263

LENGTH: 351

TYPE: PRT

ORGANISM: Homo sapiens

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US-10-482-029-263
; Sequence 263, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
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; NUMBER OF SEQ ID NOS: 24
; SOCTWARE: PATENTIN Ver. 2
; SEQ ID NO 2
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo mapiens
US-10-874-015-2
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Best Local
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LYVFVGQDFRERLIHSLPTSLERALSEDSAPTNDTAANSASPPAETELQAM
               LYVFVGQDFRERLIHSLPTSLERALSEDSAPTNDTAANSASPPAETELQAM 351
                                                                                  RVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPM
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                                                                                    LDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNF 180
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                                                              LDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNF
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Golz, Stefan

APPLICANT: Bruggemeier, Ulf

APPLICANT: Bruggemeier, Ulf

APPLICANT: Geerts, Andreas

TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with

TITLE OF INVENTION: N-Formyl Peptide Receptor Like 1 (FPRL1)

FILE REFERENCE: Le A 35 949

CURRENT APPLICATION NUMBER: US/10/509,715

CURRENT APPLICATION NUMBER: PCT/EP03/02959

PRIOR APPLICATION NUMBER: EP 02007291.4

PRIOR APPLICATION NUMBER: EP 02007291.4

PRIOR FILING DATE: 2002-04-03

NUMBER OF SEQ ID NOS: 5

SOPTWARE: Patentin version 3.3

SEQ ID NO 2

LENGTH: 351

TYPE: PRT

ORGANISM: Homo sapiens
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US-10-517-956-1
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Best Local S
Matches 351
Sequence 1, Application US/10517956
Publication No. US20050233326A1
GENERAL INFORMATION:
APPLICANT: Takeda Chemical Industries, Ltd.
TITLE OF INVENTION: Novel Screening Method
FILE REFERENCE: 3067WOOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/10509715 Publication No. US20050164305A1
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Sequence 501, Application US/09826509

Publication No. US20030204073A1

GENERAL INFORMATION:
APPLICANT: Lehmann-Bruinsma, Karin
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
ITITLE OF INVENTION: Protein-Coupled Receptors

FILE REFERENCE: AREN-207

CURRENT APPLICATION NUMBER: US/09/826,509

CURRENT FILING DATE: 2001-04-05

PRIOR APPLICATION NUMBER: 60/195,747

PRIOR APPLICATION NUMBER: 09/170,496

PRIOR APPLICATION NUMBER: 09/170,496

PRIOR FILING DATE: 1998-10-13

NUMBER OF SEQ ID NOS: 599

SEQTEMARE: Patentin Version 2.1

LENGTH: 351
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CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: UP 2002-173798
PRIOR APPLICATION NUMBER: UP 2002-205470
PRIOR APPLICATION NUMBER: UP 2002-205470
PRIOR FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 1
LENGTH: 351
TYPE: PRT
ORGANISM: Human
US-10-517-956-1
                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-501
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Score 1811; DB 3;
Pred. No. 9.6e-148;
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TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Known G
FILE REFERENCE: AREN-207
CURRENT APPLICATION NUMBER: US/10/925,095
CURRENT FILING DATE: 2004-08-24
PRIOR APPLICATION NUMBER: US/9/826,509
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US/9/826,509
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US/17,496
PRIOR FILING DATE: 1998-10-13
NUMBER: OF SEQ ID NOS: 589
SOFTWARE: Patentin Version 2.1
LENGTH: 351
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; ORGANISM: Homo sapiens
US-10-925-095-501
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US-10-925-095-501
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Best Local Similarity
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APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
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                    RVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVWPTSSLAFFNSCLNPM 300
                                                                                                   ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPL
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Pred. No. 9.6e-148;
0; Mismatches 1;
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Sequence 12, Application US/10517956
Publication No. US20050233326A1
GENERAL INFORMATION:
APPLICANT: Takeda Chemical Industries, Ltd.
TITLE OF INVENTION: Novel Screening Method
FILL REFERENCE: 3067W00P
CURRENT APPLICATION NUMBER: US/10/517,956
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: UF 2002-173798
PRIOR APPLICATION NUMBER: JP 2002-205470
PRIOR FILING DATE: 2002-06-14
PRIOR PRIOR FILING DATE: 2002-07-15
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SEQ ID NO 12
LENGTH: 351
TYPE: PRT
ORGANISM: Mouse
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US-10-517-956-12
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Best Local S
Matches 267
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                       LYVFVGQDFRERLIHSLPTSLERALSEDSAPTNDTAANSASPPAETELQA 350
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LYVFMGQDFRERFIHSLPYSLERALSEDSGQTSDSSTSSTSPPADIELKA
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                                                               RVLTAVVASFFICWFFFQLVALLGTVWFKETLLSGSYKILDMFVNPTSSLAYFNSCLNPM
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US-10-517-956-10
US-10-517-956-10
Sequence 10, Application US/10517956
Publication No. US20050233326A1
GENERAL INFORMATION:
APPLICANT: Takeda Chemical Industries, Ltd.
TITLE OF INVENTION: Novel Screening Method
FILE REFERENCE: 3067WCOP
CURRENT APPLICATION NUMBER: US/10/517,956
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: JP 2002-173798
PRIOR APPLICATION NUMBER: JP 2002-205470
PRIOR APPLICATION NUMBER: JP 2002-205470
PRIOR FILING DATE: 2002-07-15
SEQ ID NO 10
LENGTH: 351
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Sequence 118, Application US/10505486
Publication No. US20050118639A1
GENERAL INFORMATION:
APPLICANT: Takeda Chemical Industries, Ltd.
ITITLE OF INVENTION: Determination of a ligand
FILE REFERENCE: P03-00066PCT
CURRENT APPLICATION NUMBER: US/10/505,486
CURRENT FILING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: JP 2002-45728
PRIOR PILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: JP 2002-213949
PRIOR APPLICATION NUMBER: JP 2002-213949
PRIOR APPLICATION NUMBER: JP 2002-298237
PRIOR PILING DATE: 2002-07-23
PRIOR PILING DATE: 2002-07-21
PRIOR FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 233
SEQ ID NO 118
LENGTH: 591
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US-10-505-486-118
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; ORGANISM: Rat
US-10-517-956-10
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; ORGANISM: Human
US-10-505-486-118
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Best Local Similarity
Matches 255; Conserv
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Best Local Similarity
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ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPL
                                                                                                                  TICYLNLALADESFSAILEERMVSVAMREKWPFGSFLCKLVHVMIDINLEVSVYLITIIA
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                                      LDRCICVLHPAWAQNHRTMSLAKRVMTGLWIFTIVLTLPNFIFWTTISTTNGDTYCIFNF
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72.2%;
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Pred. No. 9.3e-106;
8; Mismatches 58;
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US-10-116-275-218

Sequence 218, Application US/10116275
Publication No. US20030211476A1
GENERAL INFORMATION:
APPLICANT: Blan Pharmaceutical Technoppulcant: O'Mahony, Daniel J.
APPLICANT: Brayden, David

Technology

APPLICANT:

Byrne, Daragh

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Best Local S
Matches 253
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PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 633
LENGTH: 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: ROUBH, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
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301 LYVFMGRNFQERLIRSLFTSLERALTEVPDSAQTSNTHTTSASPPEETELQAM
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                    LYVFVGQDFRERLIHSLFTSLERALSE--DSAPTNDTAANSASPPAETELQAM 351
                                                                                                                                                     ASWGGTPBERLKVAITMLTARGIIRFVIGFSLFMSIVAICYGLIAAKIHKKGMIKSSRPL
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                                                                 RVFAAVVASFFICWFPYELIGILMAVWLKEMLLNGKYKIILVLINPTSSLAFFNSCLNPI
                                                                                      RVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPM 300
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o. US20030113798A1
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APPLICANT: POWELLY DOUGLAS M.D.

APPLICANT: POWELLY DOUGLAS M.D.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING

TITLE OF INVENTION: 58305, 156, 14175, 50352, 32678, 5560, 7240, 8865, 12396,

TITLE OF INVENTION: 12397, 13644, 19938, 2077, 1735, 1786, 10220, 17822, 33945,

TITLE OF INVENTION: 43748, 47161, 81982 OR 46777

FILE REFERENCE: MPIOJ-041PJRNOWNIM

CURRENT FILLING DATE: 2004-02-27

PRIOR APPLICATION NUMBER: US 60/454,202

PRIOR APPLICATION NUMBER: US 60/454,202

PRIOR APPLICATION NUMBER: US 60/454,202

PRIOR FILLING DATE: 2003-03-12

PRIOR FILLING DATE: 2003-03-20

PRIOR APPLICATION NUMBER: US 60/465,240

PRIOR APPLICATION NUMBER: US 60/475,233

PRIOR APPLICATION NUMBER: US 60/475,233

PRIOR APPLICATION NUMBER: US 60/478,952

PRIOR APPLICATION NUMBER: US 60/478,952

PRIOR FILLING DATE: 2003-06-02

PRIOR FILLING DATE: 2003-07-16

PRIOR APPLICATION NUMBER: US 60/487,836

PRIOR FILLING DATE: 2003-09-04

NUMBER OF SEQ ID NOS: 53
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; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-275-218
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Best Local
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APPLICANT: Higgins, Lisa
TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
FILE REFERENCE: E1067/20087
CURRENT APPLICATION NUMBER: US/10/116,275
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349
SOFTWARE: PatentIn version 3.1
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Pred. No. 3.1e-105;
9; Mismatches 59; Indels
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FITILE OF INVENTION: NOVEL Screening Method
FILE REFERENCE: 3067900P
CURRENT APPLICATION NUMBER: US/10/517,956
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: JP 2002-173798
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: JP 2002-205470
PRIOR PRIOR DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 14
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US-10-517-956-14
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; ORGANISM: Homo
US-10-789-241-12
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Best Local 8
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human
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                                                        LDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNF 180
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                                                                                                              TICYLNLALADFSFSAILPFRMVSVAMREKWPFASFLCKLVHVMIDINLFVSVYLITIIA
                                ldrcicvlhpawaqnhrtmslakrvmtglwiftivltlpnfifwttisttngdtycifnf
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Length 353;

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SOFTWARE: FASTSEQ for Windows Version SEQ ID NO 12
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Search completed: March 28, 2006, 13:26:03 Job time : 216.344 secs	301 LYVFVGQDFRERLIHSLPTSLERALSEDSAPTNDTAANSASPPAETELQAM 351     : :	241 RVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPM 300 	181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPL 240 

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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/SIDS5/pcodata/1/pubpaa/USO6_NEW_PUB.pep:*
/SIDS5/pcodata/1/pubpaa/USO7_NEW_PUB.pep:*
/SIDS5/pcodata/1/pubpaa/USO7_NEW_PUB.pep:*
/SIDS5/pcodata/1/pubpaa/USO3_NEW_PUB.pep:*
/SIDS5/pcodata/1/pubpaa/USO3_NEW_PUB.pep:*
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 US-11-218-281-12
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US-11-218-281-25
US-10-508-765-2
US-11-218-281-23
US-11-218-281-2
US-11-218-281-3
US-11-218-281-3
US-11-218-281-1
US-11-218-281-1
US-11-218-281-1
US-11-218-281-3
US-11-218-281-2
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ALIGNMENTS

Sequence 12, Application US/11218281

Publication No. US20060024758A1

GENERAL INFORMATION:
APPLICANT: THE BRIGHAM AND WOMEN'S HOSPITAL, INC.
APPLICANT: Serhan, Charles N.
APPLICANT: Arita, Makoto
TITLE OF INVENTION: METHODS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY
TITLE OF INVENTION: RECEPTORS FOR EICOSAPENTAENOIC ACID ANALOGS
FILE REFERENCE: MP-14448.05

CURRENT APPLICATION NUMBER: US/11/218,281; CURRENT FILING DATE: 2005-09-01; PRIOR APPLICATION NUMBER: 60/452,244; PRIOR FILING DATE: 2003-03-05; NUMBER OF SEQ ID NOS: 33; SOFTWARE: Patentin version 3.2; SEQ ID NO 12; LENGTH: 351

TYPE: PRT ORGANISM: HOMO SAPIENS

Length

Query Match Best Local Similarity Matches 351; Conservative 241 241 181 181 121 121 LDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNF 180 61 TICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIA 120 61 TICYLNLALADESETATLEFLIVSMAMGEKWEFGWFLCKLIHIVVDINLEGSVFLIGEIA 1 METNFSTPLNEYEEVSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVT 1 METNFSTPLNEYEEVSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVT LYVFVGQDFRERLIHSLPTSLERALSEDSAPTNDTAANSASPPAETELQAM 351 RVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPM LDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNF 100.0%; Score 1817; DB 7; 100.0%; Pred. No. 2.1e-136; /ative 0; Mismatches 0; Indels 0, Gaps 300 240 240 180 120 60 60

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CURRENT FILING DATE: 2005-09-01
PRIOR APPLICATION NUMBER: 60/452,244
PRIOR FILING DATE: 2003-03-05
NUMBER OF SEQ ID NOS: 33
SOPTWARE: Patentin version 3.2
SEQ ID NO 24
LENGTH: 351
TYPE: PRT
ORGANISM: HOMO SAPIENS
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US-11-218-281-25

/ Sequence 25, Application US/11218281

/ Publication No. US20060024758A1
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Best Local S
Matches 351
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APPLICANT: THE BRIGHAM AND WOMEN'S HOSPITAL,
APPLICANT: Serhan, Charles N.
APPLICANT: Arita, Makoto
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Publication No. US20060024758A1

GENERAL INFORMATION:
AFFEICANT: THE BRIGHAM AND WOMEN'S HOSPITAL, INC.
APPLICANT: Serhan, Charles N.
APPLICANT: Serhan, Charles N.
APPLICANT: Arita, Makoto
TITLE OF INVENTION: METHODS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY
TITLE OF INVENTION: RECEPTORS FOR EICOSAPENTAENOIC ACID ANALOGS
TITLE OF INVENTION: METHODS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY TITLE OF INVENTION: RECEPTORS FOR EICOSAPENTAENOIC ACID ANALOGS FILE REFERENCE: MP-14448.05
CURRENT APPLICATION NUMBER: US/11/218,281
CURRENT FILING DATE: 2005-09-01
PRIOR APPLICATION UMMBER: 60/452,244
PRIOR FILING DATE: 2003-03-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.2
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CURRENT APPLICATION NUMBER: US/11/218,281
CURRENT FILING DATE: 2005-09-01
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; TYPE: PRT
; ORGANISM: Homo sapiens
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PRIOR FILING DATE: 2003-03-10
PRIOR APPLICATION NUMBER: EP 02006595.9
PRIOR FILING DATE: 2002-03-22
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.3
SEQ ID NO 2
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LENGTH:
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APPLICANT: Golz, Stefan
APPLICANT: Bruggemeier, Ulf
APPLICANT: Bruggemeier, Ulf
APPLICANT: Geerts, Andreas
TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with Homo
TITLE OF INVENTION: Sapiens Formyl Peptide Receptor-Like 2
FILE REFERENCE: Le A 35 838
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Best Local S
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CURRENT FILING DATE: 2004-09-22
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 121 LDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNF 180
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                                                                                                                                                                               h 72.5*; Score 1318; DB 6; Similarity 71.7*; Pred. No. 5.2e-97; 53; Conservative 39; Mismatches 59)
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                                                        TICYLNLALADFSFTATLFFLIVSMAMGEKWFFGWFLCKLIHIVVDINLFGSVFLIGFIA 120
                                                                                                           METNESIPLNETEEVLPEPÄGHTVLWIFSLLVHGVTFVFGVLGNGLVIWVÄGERMTRTVN 60
                                                                                                                                  METNFSTPLNEYEEVSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVT 60
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                                                                                                                                                                                     59;
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                                                                                                                                                                                                                     Length 353;
                                                                                                                                                                                   Indels
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CURRENT APPLICATION NUMBER: US/11/218,281
CURRENT FILING DATE: 2005-09-01
PRIOR APPLICATION NUMBER: 60/452,244
PRIOR FILING DATE: 2003-03-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 23
LENGTH: 350
TYPE: PRT
ORGANISM: HOMO SAPIENS
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US-11-218-281-23
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RESULT 6
US-11-218-281-27
; Sequence 27, Application US/11218281
; Publication No. US20060024758A1
; GENERAL INFORMATION:
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APPLICANT: THE BRIGHAM AND WOMEN'S HOSPITAL, INC.
APPLICANT: Serhan, Charles N.
APPLICANT: Serhan, Charles N.
APPLICANT: Arita, Makoto
TITLE OF INVENTION: METHODS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY
TITLE OF INVENTION: RECEPTORS FOR BICOSAPENTAENOIC ACID ANALOGS
FILE REFERENCE: MP-14448.05
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Best Local (
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                                                                                                                    LYVFMGQDFRERLIHALPASLERALTEDSTQTSDTATNSTLPSAEVALQA
                                                                                                                                    LYVFVGQDFRERLIHSLFTSLERALSEDSAPTNDTAANSASFPAETELQA 350
                                                                                                                                                                                    RVLSFVAAAFFLCWSPYQVVALIATVRIRELL-QGMYKBIGIAVDVTSALAFFNSCLNPM
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; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-11-218-281-27
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US-11-134-811-4
              CURRENT FILING DATE: 2005-05-20
PRIOR APPLICATION NUMBER: 10/603,566
PRIOR APPLICATION NUMBER: 10/603,566
PRIOR PILING DATE: 2003-06-25
PRIOR PPLICATION NUMBER: US 60/303,858
PRIOR PPLICATION NUMBER: US 60/303,858
PRIOR PPLICATION NUMBER: US 09/905,253
PRIOR PPLICATION NUMBER: US 09/905,253
PRIOR PILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 10/201,187
PRIOR APPLICATION NUMBER: US 10/201,187
PRIOR PILING DATE: 2001-07-23
PRIOR PILING DATE: 2001-07-3
PRIOR PILING DATE: 2002-07-09
NUMBER OF SEQ ID NOS: 94
                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Wittamer, Valerie
APPLICANT: Communi, David
APPLICANT: Vandenbogaerde, Ann
APPLICANT: Detheux, Michel
APPLICANT: Parmentier, Marc
APPLICANT: Parmentier, Marc
TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
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Best Local Similarity
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CURRENT FILING DATE: 2005-09-01
PRIOR APPLICATION NUMBER: 60/452,244
PRIOR FILING DATE: 2003-03-05
NUMBER OF SEQ ID NOS: 33
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APPLICANT: Arita, Makoto
TITLE OF INVENTION: METHODS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY
TITLE OF INVENTION: RECEPTORS FOR EICOSAPENTAENOIC ACID ANALOGS
FILE REFERENCE: MP-14448
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                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 9409/2043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276
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PatentIn version 3.1
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CURRENT APPLICATION NUMBER: US/11/218,281
CURRENT FILING DATE: 2005-09-01
PRIOR APPLICATION NUMBER: 60/452,244
PRIOR FILING DATE: 2003-03-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 2
LENGTH: 371
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                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: MOUSE
US-11-218-281-2
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US-11-218-281-2
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                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 120; Conserv
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APPLICANT: THE BRIGHAM AND WOMEN'S HOSPITAL, INC.
APPLICANT: Serhan, Charles N.
APPLICANT: Arita, Makoto
TITLE OF INVENTION: METHODS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY
TITLE OF INVENTION: RECEPTORS FOR EICOSAPENTAENOIC ACID ANALOGS
FILE REFERENCE: MP-14448.05
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Best Local Similarity
Matches 120; Conserv
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ORGANISM: Mus musculus
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                    122 DRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNFA 181
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                                                                                                                ICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIAL 121
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DRCISVLLPVWSQNHRSIRLAYMTCSAVWVLAFFLSSPSLVFRDTANI-HGKITCFNNFS
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                                                                                                                                                                                                                                 29.6%; Score 538.5; DB 7;
35.2%; Pred. No. 1.9e-35;
rative 70; Mismatches 124;
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PRIOR APPLICATION NUMBER: 60/452,244
PRIOR FILING DATE: 2003-03-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.2
SEQ ID NO 3
LENGTH: 371
TYPE: PRT
ORGANISM: MOUSE
US-11-218-281-33
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APPLICANT: THE BRIGHAM AND WOMEN'S HOSPITAL,
APPLICANT: Serhan, Charles N.
APPLICANT: Arita, Makoto
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Best Local Similarity 35.2
Matches 120; Conservative
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CURRENT FILING DATE: 2005-09-01
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Local Similarity 35.2%; Pred. No. 1.9e-35;
nes 120; Conservative 70; Mismatches 124;
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                 FNSCLNPMLYVFVGQDFRERLIHSLPTSLERALSEDSAPTN 333
                                                                                AKNKKPFKIITIIITFFLCWCPYH-----TLYLLELHHTAVPSSVFSLGLPLATAVAI
                                                                                                        IKSSRPLRVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNP-TSSLAF 292
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                                                                                                                                                                                    SWGGTPEERLKVAITMLTARG------IIRPVIGFSLPMSIVAICYGLIAAKIHKKGM 233
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ANSCMNPILYVEMGHDERKFKV-ALFSRLANALSEDTGPSS 344
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ANSCMNPILYVFMGHDFRKFKV-ALFSRLANALSEDTGPSS 344
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RESULT 10
US-11-134-811-2
; Sequence 2, Application US/11134811
; Publication No. US20060024750A1
; GENERAL INFORMATION:
; APPLICANT: Wittamer, Valerie
; APPLICANT: Communi, David

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NUMBER OF SEQ ID NOS: 94
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 371
TYPE: PRT
                                                                                                                                                                                                                                                                                    Sequence 1, Application US/11218281
Publication No. US20060024758A1
GENERAL INFORMATION:
APPLICANT: THE BRIGHAM AND WOMEN'S HOSPITAL,
APPLICANT: Serhan, Charles N.
APPLICANT: Arita, Makoto
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 373
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                                                                          TITLE OF INVENTION: METHODS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY TITLE OF INVENTION: RECEPTORS FOR BICOSAPENTAENOIC ACID ANALOGS FILE REPERENCE: MP-14448.05 CURRENT APPLICATION NUMBER: US/11/218,281 CURRENT FILING DATE: 2005-09-01 PRIOR APPLICATION NUMBER: 60/452,244 PRIOR PILING DATE: 2003-03-05 NUMBER: 07.03-05 NUMBER: 07.03-05 SEQ ID NOS: 33
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PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 09/905,253
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 10/201,187
PRIOR FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: PCT/EP02/0764*
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PRIOR FILING DATE: 2003-06-25
PRIOR APPLICATION NUMBER: US 60/303,858
PRIOR FILING DATE: 2001-07-09
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CURRENT FILING DATE: 2005-05-20
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TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
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Local Similarity 36.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 YHTLNLLE---LHHTAMPG--SVFSLGLPLATALAIANSCMNPILYVFMGQDFKKFKV-A 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197 MLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVLTAVVASFFICWFP
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Pred. No. 3.9e-35;
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; TYPE: PRT
; ORGANISM: H
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; ORGANISM: HOMO SAPIENS
US-11-218-281-28
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SEQ ID NO 28
LENGTH: 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28, Application US/11218281 Publication No. US20060024758A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 29.4%; Score 534.5; DB 7
Best Local Similarity 36.3%; Pred. No. 3.9e-35;
Matches 122; Conservative 65; Mismatches 130
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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CURRENT FILING DATE: 2005-09-01
PRIOR APPLICATION NUMBER: 60/452,244
PRIOR FILING DATE: 2003-03-05
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHODS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY TITLE OF INVENTION: RECEPTORS FOR EICOSAPENTAENOIC ACID ANALOGS FILE REFERENCE: MP-14448.05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Serhan, Charle APPLICANT: Arita, Makoto
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                                          158 MACMVIWVLAFFLSSPSLVFRDTANL-HGKISCFNNFSLSTPGSSSW-PTHSQMDPVGYS
                                                                                      144 KVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNF-----ASWGGTPBERLKVAIT 196
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MLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVLTAVVASFFICWFP
                                                                                                                                     YAAMDYHWVFGTAMCKISNFLLIHMMFTSVFLLTIISSDRCISVLLPVWSQNHRSVRLAY 157
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US-11-169-976-9
Sequence 9, Application US/11169976
Publication No. US20060014249A1
GENERAL INFORMATION:
APPLICANT: Li, et al.
APPLICANT: Li, et al.
TITLE OF INVENTION: Human G-Protein Coupled Receptor;
FILE REFERENCE: PF159P1C2
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CURRENT APPLICATION NUMBER: US/10/502,145
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: USSN 60/350,961
PRIOR FILING DATE: 2002-01-25
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
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Publication No. US20050244406A1
GENERAL INFORMATION:
APPLICANT: MACKAY, CHARLES REAY
TITLE OF INVENTION: Anti-C5aR antibodies and
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ORGANISM: Homo sapiens
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PRIOR APPLICATION NUMBER: 10/259,521
PRIOR FILLYG DATE: 2002-09-30
PRIOR APPLICATION NUMBER: 08/462,314
PRIOR FILLYG DATE: 1995-06-05
PRIOR APPLICATION NUMBER: PCT/US95/01992
PRIOR FILLYG DATE: 1995-02-17
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.2
SEQ ID NO 9
SEQ ID NO 9
SEQ ID NO 9
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                                                                                                                                                                                                                                                                                                                                                                                       Sequence 31, Application US/11218281 Publication No. US20060024758A1 GENERAL INFORMATION:
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Best Local S
Matches 122
                                                                                                                        SEQ ID NO 31
  Query Match
                                                                                                                                                                                                                                                               APPLICANT: THE BRIGHAM AND WOMEN'S HOSPITAL, INC.
APPLICANT: Serhan, Charles N.
APPLICANT: Arita, Makoto
TITLE OF INVENTION: METHODS FOR IDENTIFICATION AND USES OF ANTI-INFLAMMATORY
TITLE OF INVENTION: RECEPTORS FOR EICOSAPENTAENOIC ACID ANALOGS
FILE REFERENCE: MP-14448.05
                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/11/218,281
CURRENT FILING DATE: 2005-09-01
PRIOR APPLICATION NUMBER: 60/452,244
PRIOR FILING DATE: 2003-03-05
                                                                                                                                         NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn versi
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ORGANISM: HOMO
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		PISLER  :   PSLLRN	LLGTVW	GIIRFV  :    AIVRLV	GPWILA:	GEKWPF	LPLVVI     :   ALVIF	Pred. No. 1.8e-33; 60; Mismatches 129;
		ALSED  : : VLTEE	LKEMI.  MS	IGFSL :   LGFLW	FILTI  :  :  vLTL	GWFLC	GVTFV  - : AVVFL	Indels
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US-10-029-386-32192	US-09-864-761-41658	US-09-864-761-33314	US-10-029-386-33584	US-10-437-963-188777	US-10-425-115-248503	US-09-925-300-1762	US-10-514-653-11	US-10-517-956-9	US-10-514-653-23	US-10-514-653-13	US-10-517-956-5	US-10-481-044-4	US-10-517-956-7	US-10-517-956-8	US-10-514-653-25	US-10-514-653-22	US-10-514-653-21
Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Seguence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
32192, A	41658, A	33314, A	33584, A	188777,	248503,	1762, Ap	11, Appl	9, Appli		13, Appl	5, Appli	4, Appli	7, Appli	8, Appli	25, Appl	22, Appl	•

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## ALIGNMENTS

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GENERAL INFORMATION:

GENERAL INFORMATION: Differentially Regulated Prostate Cancer Genes

TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes

FILE REFERENCE: 9U 204 205 R1

CURRENT APPLICATION NUMBER: US/10/341,434

CURRENT FILING DATE: 2003-07-18

PRIOR APPLICATION NUMBER: US 60/348,164

PRIOR FILING DATE: 2002-01-15

PRIOR FILING DATE: 2002-01-15

PRIOR FILING DATE: 2002-01-15

NUMBER OF SEQ ID NOS: 238

SOPTWARE: PatentIn version 3.1

SEQ ID NO 167

LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Reed, John C.

APPLICANT: Guo, Bin
TITLE OF INVENTION: Methods for Identifying Modulators of
TITLE OF INVENTION: Apoptosis
FILE REFERENCE: P-LJ 5535
CURRENT APPLICATION NUMBER: US/10/306,878
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: US 60/334,149
PRIOR FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: (28)
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                            RESULT 2
US-10-341-434-167
US-10-341-434-167
Sequence 167, Application US/10341434
Publication No. US20030215835A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-306-878-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/10306878 Publication No. US20030175819A1 GENERAL INFORMATION:
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Pred. No. 8.1e-12;
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US-10-341-434-167
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US-10-341-434-200
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FILE REFERENCE: 9U 204 205 R1
CURRENT APPLICATION NUMBER: US/10/341,434
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/348,164
PRIOR FILING DATE: 2002-01-15
SOUTWARE: Patentin version 3.1
SEQ ID NO 200
LENGTH: 24
TYPE: PRT
           Best Loc
Matches
                                                                                                             SOFTWARE: PatentIn version 3.3
SEQ ID NO 1
LENGTH: 24
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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                                                   Query Match
                                                                                                                                                                                                        APPLICANT: SAKANOUE, Kenji
APPLICANT: ITOH, Chika
APPLICANT: ITOH, Chika
APPLICANT: YASUKOHCHI, Tohru
TITLE OF INVENTION: MODIFIED BIO-RELATED SUBSTANCE, PROCESS FOR PRODUCING THE SAME,
TITLE OF INVENTION: AND INTERMEDIATE
TITLE OF INVENTION: AND INTERMEDIATE
TITLE OF INVENTION: AND INTERMEDIATE
TITLE REFERENCE: Q78575
CURRENT APPLICATION NUMBER: US/10/716,432
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: JP 2003-337113
PRIOR APPLICATION NUMBER: JP 2003-337113
PRIOR PILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 1
COCCUMANCE: DEFENTIN US/10 1 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: NOF COTP.
APPLICANT: NAKAMOTO, Ken-ichiro
APPLICANT: OHASHI, Syunsuke
APPLICANT: YAMAMOTO, Yuji
APPLICANT: SAKANOUE, Kenji
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Local 5.
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                               Similarity
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5. US20030215835A1
      100.0%; Score 120; DB 5; ilarity 100.0%; Pred. No. 8.1e-12; Conservative 0; Mismatches 0;
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Sequence 3, Application US/10517956
Publication No. US20050233326A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Takeda Chemical Industries, Ltd.
TITLE OF INVENTION: NOVel Screening Method
FILE REFERENCE: 3067MO0P
CURRENT APPLICATION NUMBER: US/10/517,956
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: JP 2002-173798
PRIOR FILING DATE: 2002-06-14
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                                                                                                                                                                                              PRIOR APPLICATION NUMBER: JP 2002-205470
PRIOR FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 3
LENGTH: 24
TYPE: PRT
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CURRENT FILING DATE: 2004-05-24
PRIOR APPLICATION NUMBER: EP01204600.9
PRIOR FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 55
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 2
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                                                                           Matches
                                                                                                                   Query Match
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Best Local Similarity
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                            ORGANISM: Human
                                                                                                  Local Similarity
                                 1 MAPRGFSCLLLLTSBIDLPVKRRA 24
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MAPRGFSCLLLLTSEIDLPVKRRA 24
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                                                                               Conservative
                                                                                                100.0%; Score 120; DB 5; 100.0%; Pred. No. 8.1e-12;
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                                                                                                                   Length 24;
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; Sequence 1, Application US/10514653 ; Publication No. US20050233413A1 ; GENERAL INFORMATION: APPLICANT: Nishimoto, Ikuo

RESULT 7 US-10-514-653-1

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; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-514-653-1
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US-10-514-653-5
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                                                                                                                             Sequence 5, Application US/10514653 Publication No. US20050233413A1 GENERAL INFORMATION:
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                  APPLICANT: Nishimoto, Ikuo
TITLE OF INVENTION: NEUROPROTECTIVE POLYPEPTIDES AND METHODS OF USE
FILE REFERENCE: 14143-002US1
CURRENT APPLICATION NUMBER: US/10/514,653
CURRENT FILING DATE: 2004-11-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/JP03/06139
PRIOR FILING DATE: 2003-05-16
PRIOR APPLICATION NUMBER: US 60/380,958
PRIOR FILING DATE: 2002-05-16
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/JP03/06139
PRIOR FILING DATE: 2003-05-16
PRIOR APPLICATION NUMBER: US 60/380,958
PRIOR FILING DATE: 2002-05-16
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.1
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CURRENT FILING DATE: 2004-11-15
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TITLE OF INVENTION: NEUROPROTECTIVE POLYPEPTIDES AND METHODS OF USE
FILE REFERENCE: 14143-002US1
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CURRENT FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: PCT/JP03/06139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MISC_FEATURE
LOCATION: (14)...(14)
OTHER INFORMATION: The 'Ser'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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US-10-514-653-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/10514653 Publication No. US20050233413A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.1 SEQ ID NO 5
                                                                    Matches
                                                                                                 Query Match
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NEUROPROTECTIVE POLYPEPTIDES AND METHODS OF USE FILE REFERENCE: 14143-002US1
CURRENT APPLICATION NUMBER: US/10/514,653
CURRENT FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: PCT/JP03/06139
PRIOR FILING DATE: 2003-05-16
PRIOR FILING DATE: 2003-05-16
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/380,958 PRIOR FILING DATE: 2002-05-16
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PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2002-05-16
NUMBER OF SEQ ID NOS: 27
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                                                                                                                                                                                                                           NAME/KBY: MISC FEATURE LOCATION: (7)...(7)
OTHER INFORMATION: The
                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial
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NAME/KEY: MISC FEATURE
LOCATION: (7)...(7)
OTHER INFORMATION: The 'Ser' at location 7 stands
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ORGANISM: Artificial
FEATURE:
                                                                                                                                                                       NAME/KEY: MISC FEATURE LOCATION: (14)..(14)
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                                                           n 100.0%; Score 120; DB 5; Similarity 100.0%; Pred. No. 8.1e-12; 24; Conservative 0; Mismatchae ^-
                    MAPRGFSCLLLLTSEIDLPVKRRA 24
MAPRGFSCLLLLTSEIDLPVKRRA
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Pred. No. 8.1e-1
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RESULT 11 US-10-514-653-7

Sequence 7, Application US/10514653 Publication No. US20050233413A1 GENERAL INFORMATION:

APPLICANT: Nishimoto,

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APPLICANT: NISHINGTO, IKUG
APPLICANT: NISHINGTO, IKUG
TITLE OF INVENTION: NEUROPROTECTIVE POLYPEPTIDES AND MET
FILE REFERENCE: 14143-002US1
CURRENT APPLICATION NUMBER: US/10/514,653
CURRENT FILING DATE: 2004-11-15
PRIOR PELLING DATE: 2003-05-16
PRIOR PILING DATE: 2003-05-16
PRIOR APPLICATION NUMBER: US 60/380,958
PRIOR APPLICATION NUMBER: US 60/380,958
PRIOR FILING DATE: 2002-05-16
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 24
TYPE: PRT
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; LOCATION: (14) ... (14)
; OTHER INFORMATION: The 'Ser' at location 14 stands
US-10-514-653-7
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US-10-514-653-9
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; LENGTH: 24
; TYPE; PRT
; ORGANISM: Artificial
; FEATURE:
Sequence 9, Application US/10514653 Publication No. US20050233413A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/10514653
Publication No. US20050233413A1
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/514,653
CURRENT FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: PCT/JP03/06139
PRIOR FILING DATE: 2003-05-16
PRIOR APPLICATION NUMBER: US 60/380,958
PRIOR APPLICATION NUMBER: US 60/380,958
PRIOR FILING DATE: 2002-05-16
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SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NEUROPROTECTIVE POLYPEPTIDES AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MISC_FEATURE
LOCATION: (7)...(7)
OTHER INFORMATION: The 'Ser' at location 7 stands for D-Ser
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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Similarity 100.0%;
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Pred. No. 8.1e-12;
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CURRENT APPLICATION NUMBER: US/10/514,653
CURRENT FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: PCT/JP03/06139
PRIOR FILING DATE: 2003-05-16
PRIOR APPLICATION NUMBER: US 60/380,958
PRIOR FILING DATE: 2002-05-16
PRIOR FILING DATE: 2002-05-16
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 24
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                                                                                                                                                                                                         PRIOR FILING DATE: 2002-05-16
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 24
                                                                                               Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NEUROPROTECTIVE POLYPEPTIDES FILE REFERENCE: 14143-002051 CURRENT APPLICATION NUMBER: US/10/514,653 CURRENT FILING DATE: 2004-11-15
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TITLE OF INVENTION: NEUROPROTECTIVE POLYPEPTIDES AND METHODS OF USE
FILE REFERENCE: 14143-002US1
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Nishimoto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MISC FEATURE LOCATION: (14)...(14) OTHER INFORMATION: The 'Ser' at location 14 stands for D-Ser.
                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: MISC_FEATURE
LOCATION: (7)...(7)
OTHER_INFORMATION: The 'Ser'
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                                                                                               Similarity
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MAPRGFSCLLLLTSEIDLPVKRRA 24
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                                                                         100.0%; Score 120; DB 5;
100.0%; Pred. No. 8.1e-12
tive 0; Mismatches 0
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US-10-514-653-17
Sequence 17, Application US/10514653
; Dublication No. US20050233413A1
; GENERAL INFORMATION:
; APPLICANT: Nishimoto, Ikuo

RESULT 15

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FILE REFERENCE: 14143-002US1
FILE REFERENCE: 14143-002US1
CURRENT APPLICATION NUMBER: US/10/514,653
CURRENT FILING DATE: 2004-11-15
PRIOR FILING DATE: 2004-11-15
PRIOR FILING DATE: 2004-11-15
PRIOR FILING DATE: 2004-11-15
PRIOR FILING DATE: 2003-05-16
PRIOR FILING DATE: 2003-05-16
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PRIOR FILING DATE: 2002-05-16
PRIOR FILING DATE: 2002-05-16
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PRIOR FILING DATE: 2004-
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Maximum Match 100%
Listing first 45 summaries
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DB seq length: 2000000000
Published Applications AA New:*

1: /SIDSS/ptodata/1/pubpaa/USO8 NEW PUB.pep:*

2: /SIDSS/ptodata/1/pubpaa/USO7 NEW PUB.pep:*

3: /SIDSS/ptodata/1/pubpaa/USO7 NEW PUB.pep:*

4: /SIDSS/ptodata/1/pubpaa/USO7 NEW PUB.pep:*

5: /SIDSS/ptodata/1/pubpaa/USO5 NEW PUB.pep:*

6: /SIDSS/ptodata/1/pubpaa/USO5 NEW PUB.pep:*

7: /SIDSS/ptodata/1/pubpaa/USO5 NEW PUB.pep:*

8: /SIDSS/ptodata/1/pubpaa/USO5 NEW PUB.pep:*
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120
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match	Len	DB 7	ID US-11-142-255-1	Description
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ω	42	35.0	345	7	-11-096-568A-356	Sequence
4	42	•	542	٥	-10-507-	Seguence
G	40.5	33.8	282	0	-10-517-	Sequence
თ	40	33.3	24	თ	-064-45	Sequence
7	40	33.3	24	7	-11-129-741-	Seguence
8	40	33.3	24	7	-11-129-741	Sequence
9	40		79	0	-10-746-909-	Sequence
10	40		157	0	US-10-980-388-73	Sequence
11	40		157	7	US-11-087-099-647	Sequence
12	40	33.3	178	6	-10-511-538-	Seguence
13	40	33.3	194	7	US-11-087-099-3269	Sequence
14	39		44	0	US-10-467-657-6070	Sequence
15	39	٠	74	7	US-11-123-896-59	Sequence
16	39	٠	74	7	US-11-123-896-62	Sequence
17	39	•	74	7	÷	Sequence
18	39	32.5	74	7	US-11-123-896-68	Sequence
19	39	٠	84	7	US-11-096-568A-4498	Sequence
20	39	٠	104	7	US-11-096-568A-4497	Sequence
21	39	•	189	7	US-11-107-029-4	Sequence
22	39	•	311	σ	-10-980	Seguence
23	39		311	0	-10-980	Sequence
24	39	32.5	530	6	US-10-980-388-62	Seguence
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<b>4</b> 5	44	43	42	41	40	39	38	37	36	35	ω 4	33	32	31	30	29	28	27	
38	38	38	38	38	38	38	38	38	38	38	38	38	38	38.5	38.5	38.5	38.5	38.5	,
31.7	31.7	31.7	31.7	31.7	31.7	31.7	31.7	31.7	31.7	31.7	31.7	31.7	31.7	32.1	32.1	32.1	32.1	32.1	(1:1
384	335	331	250	250	248	191	191	184	166	166	152	152	121	332	316	154	95	92	•
7	7	7	σ	σ	თ	7	7	7	7	7	7	7	σ	7	7	σ	7	7	•
US-11-087-099-6378	US-11-182-946-7	US-11-185-878-3	US-10-973-115B-320	US-10-131-826A-320	US-10-644-807-326	US-11-096-568A-25506	US-11-096-568A-675	US-11-096-568A-12134	US-11-096-568A-25507	US-11-096-568A-676	US-11-096-568A-25508	US-11-096-568A-677	US-10-644-807-410	US-11-074-176-230	US-11-074-176-358	US-10-793-626-602	US-11-096-568A-2283	US-11-096-568A-2284	** ** *** ****
Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	00440000
6378, Ap	7, Appli	3, Appli	320, App	320, App	326, App	25506, A	675, App	12134, A	25507, A	676, App	25508, A	677, App	410, App	230, App	358, App	602, App	2283, Ap	2284, Ap	The same

## ALIGNMENTS

RESULT 1 US-11-142-255-1

Sequence 1, Application US/11142255 Publication No. US20050288490A1 GENERAL INFORMATION:

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RESULT 4
US-10-507-755-6
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Best Local S
Matches 9
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 356, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 13754
LENGTH: 256
              SEQ ID NO 6
LENGTH: 542
                                                                                                                                                                                                                                                                                   Sequence 6, Application US/10507755 Publication No. US20060051754A1 GENERAL INFORMATION:
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ORGANISM: Zea mays subsp. m
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(256)
OTHER INFORMATION: Ceres Se
                                              APPLICANT: ENDOU, HITOSHI
APPLICANT: KANAI, YOSHIKATSU
APPLICANT: KANAI, YOSHIKATSU
TITLE OF INVENTION: TRANSPORTER SELECTIVELY TRANSPORTING SULFATE CONJUGATE
TITLE OF INVENTION: AND ITS GENE
FILE REFERENCE: 61552(71526)
CURRENT APPLICATION NUMBER: US/10/507,755
CURRENT FILING DATE: 2005-09-14
PRIOR APPLICATION NUMBER: FCT/JF03/02980
PRIOR FILING DATE: 2003-03-13
PRIOR FILING DATE: 2003-03-14
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 3.3
LENGTH: 5.
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Zea mays subsp. mays FEATURE:
FEATURE: misc_feature
LOCATION: (1)...(345)
OTHER INFORMATION: Ceres Seq. ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 345
TYPE: PRT
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36.4%;
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Pred. No. 24;
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RESULT 6
US-10-895-064-459
; Sequence 459, Application US/10895064
; Publication No. US20060018923A1
; GENERAL INFORMATION:
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Best Local Similarity
Marches 9; Conserve
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SOUTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 346

SEQ ID NO 346

LENGTH: 282

TYPE: PRT
ORGANISM: Unknown
FEATURE:
FEATURE:
OTHER IMPORMATION: Obtained from an environmental sample.
US-10-517-939-346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens US-10-507-755-6
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FILE REPERENCE: V0690.0031
CURRENT APPLICATION NUMBER: US/10/895,064
CURRENT FILING DATE: 2004-07-21
NUMBER OF SEQ ID NOS: 2918
SOFTWARE: Patentin version 3.2
SEQ ID NO 459
LENGTH: 24
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                                                                                                                       APPLICANT: CHAN, KWOK HUNG
APPLICANT: NICHOLLS, JOHN M.
APPLICANT: LEUNG, FREDERICK C.
APPLICANT: LEUNG, FREDERICK C.
TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT INFECTION AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/517,939
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/US03/19153
PRIOR FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/389,299
PRIOR FILING DATE: 2002-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Blum, David
APPLICANT: Esteghlalian, Alireza
TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS
TITLE OF INVENTION: AND METHODS FOR MAKING
FILE REFERENCE: 564462007901
                                                                                                                                                                                                                                               APPLICANT: PEIRIS,
APPLICANT: YUEN, I
                                                                                                                                                                                                                APPLICANT:
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hes 8; Conserv
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Healey, Shaun
                                                                                                                                                                                                                                                   YUEN, KWOK YUNG
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72.7%;
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Pred.
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Query Match
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Thes 9; Conserva
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US-11-129-741-459
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; ORGANISM: Corononavirus-HKU1
US-10-895-064-459
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US-11-129-741-459
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TITLE OF INVENTION: INFECTION AND USES THEREOF
FILE REFERENCE: V0690.0044
CURRENT APPLICATION NUMBER: US/11/129,741
CURRENT FILING DATE: 2005-05-16
PRIOR APPLICATION NUMBER: 10/895,064
PRIOR APPLICATION NUMBER: 10/895,064
PRIOR FILING DATE: 2004-07-21
NUMBER OF SEQ ID NOS: 4257
SOPTWARE: Patentin version 3.3
SEQ ID NO 459
LENGTH: 24
TYPE: PRT
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Best Local Similarity
Matches 9; Conserv
SEQ ID NO 3477
LENGTH: 24
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                           TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
TITLE OF INVENTION: INFECTION AND USES THEREOF
FILE REFERENCE: V0690.0044
CURRENT APPLICATION NUMBER: US/11/129,741
CURRENT FILING DATE: 2005-05-16
PRIOR APPLICATION NUMBER: 10/895,064
PRIOR APPLICATION NUMBER: 10/895,064
PRIOR FILING DATE: 2004-07-21
NUMBER OF SEQ ID NOS: 4257
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 459, Publication No.
                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION
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WOO, CHIU YAT PATRICK
LAU, KAR PUI SUSANNA
CHAN, KWOK HUNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YUEN, KWOK YUNG
WOO, CHIU YAT PATRICK
LAU, KAR PUI SUSANNA
CHAN, KWOK HUNG
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PEIRIS, JU
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b. US20060034853A1
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Pred. No. 3;
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; ORGANISM: Corononavirus-HKU1
US-11-129-741-3477
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CURRENT APPLICATION NUMBER: US/10/980,388
CURRENT FILING DATE: 2004-11-02
PRIOR APPLICATION NUMBER: US/09/791,932
PRIOR FILING DATE: 2001-02-3
PRIOR APPLICATION NUMBER: 60/184,305
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/184,304
PRIOR APPLICATION NUMBER: 60/184,304
PRIOR APPLICATION NUMBER: 60/184,304
PRIOR APPLICATION NUMBER: 60/184,304
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US-10-746-909-10
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CURRENT FILING DATE: 2003-12-23
PRIOR APPLICATION NUMBER: 08/175,071
PRIOR FILING DATE: 1993-12-29
PRIOR APPLICATION NUMBER: 08/107,332
PRIOR FILING DATE: 1993-08-16
PRIOR APPLICATION NUMBER: 07/580,655
PRIOR APPLICATION NUMBER: 07/580,655
PRIOR APPLICATION NUMBER: 07/580,655
PRIOR APPLICATION NUMBER: 07/580,655
PRIOR FILING DATE: 1990-09-11
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SEQ ID NO 10
LENGTH: 79
                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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Publication No. US20060008873A1
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                                                                                                                                                           APPLICANT: Ruff, Valerie
APPLICANT: Huff, Rita M.
APPLICANT: Wood, Linda S.
TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference
FILE REFERENCE: 00325.US1
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Best Local :
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APPLICANT: Chus, Kaw-yan
TITLE OF INVENTION: CLONING AND SEQUENCING OF ALLERGENS OF
TITLE OF INVENTION: DERMATOPHAGOIDES (HOUSE DUST MITE)
                                                                                                                                                                                                                                                                                            APPLICANT: Vogeli, Gabriel
APPLICANT: Parodi, Luis A
APPLICANT: Hiebsch, Ronald
APPLICANT: Lind, Peter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 07/458,642
PRIOR FILING DATE: 1990-02-13
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TYPE: PRT
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Hiebsch, Ronald R.
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Pred. No.
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Pred. No.
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RESULT 11
US-11-087-099-647
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US-10-980-388-73
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SEQ ID NO 647
LENGTH: 157
TYPE: PRT
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Publication No. US20060026700A1
GENERAL INFORMATION:
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Matches 9; Conserv
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APPLICANT: Abad, Ma
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                                APPLICANT: Origene Technologies, Inc
TITLE OF INVENTION: TISSUE SPECIFIC GENES AND GENE CLUSTERS
FILE REFERENCE: 16U 200 PCT
CURRENT APPLICATION NUMBER: US/10/511,538
CURRENT FILING DATE: 2004-10-18
PRIOR APPLICATION NUMBER: US 66/372,669
PRIOR PILING DATE: 2002-04-16
PRIOR PILING DATE: 2002-04-16
PRIOR PILING DATE: 2002-04-16
PRIOR PILING DATE: 2002-09-20
PRIOR FILING DATE: 2002-09-20
PRIOR FILING DATE: 2002-09-20
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PRIOR APPLICATION NUMBER: 60/218,492
PRIOR FILING DATE: 2000-07-20
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Genes and Uses for Plant Improvement FILE REPERENCE: 38-21 (53450)B EP CURRENT APPLICATION NUMBER: US/11/087,099

CURRENT FILING DATE: 2005-03-22
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Local Similarity 53.3%;
nes 8; Conservative
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PR FILING DATE: 2000-02-23

PR PILING DATE: 2000-03-13

PR FILING DATE: 2000-03-13

PR APPLICATION NUMBER: 60/217,369

PR APPLICATION NUMBER: 60/217,370

PR APPLICATION NUMBER: 60/217,370
APPLICATION NUMBER: US 60/424,336 FILING DATE: 2002-11-07
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APPLICATION NUMBER: 60/184,397
FILING DATE: 2000-02-23
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                                                                                                                                                                                                                                                    Application US/10511538
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o. US20060041961A1
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llarity 56.2%;
Conservative
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Pred. No. 22;
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US-10-511-538-85
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PRIOR FILING DATE: 2002-08-16
NUMBER OF SEQ ID NOS: 344
SOFTWARE: PatentIn version 3.1
SEQ ID NO 85
LENGTH: 178
                                                     NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SegWin99, versio
SEQ ID NO 6070
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Publication No. US20050260581A1
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LENGTH: 194
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Best Local (
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Best Local :
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                                                                                                           CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
                                                                                                                                                                                                   APPLICANT: CHIRON SPA
APPLICANT: FONTANA MARIAGIRATIA
APPLICANT: PIZZA MARIAGIRAZIA
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Abad, Mark S. et al.

TITLE OF INVENTION: Genes and Uses for Plant Improvement FILE REFERENCE: 38-21(53450) B. CURRENT APPLICATION NUMBER: US/11/087,099

CURRENT FILING DATE: 2005-03-22

NUMBER OF SEQ ID NOS: 12464
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PRIOR PILING DATE: 2002-05-01
PRIOR APPLICATION NUMBER: US 60/381,366
PRIOR FILING DATE: 2002-05-20
                                                                                                                                                                                      FILE REFERENCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Triticum aestivum
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ORGANISM: Neisseria gonorrhoeae
                                    LENGTH: 44
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Pred. No.
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Pred. No.
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Sequence 59, Application US/11123896

Publication No. US20050273881A1

GENERAL INFORMATION:

APPLICANT: Simmons, Carl R.

APPLICANT: Simmons, Carl R.

APPLICANT: Navarro Acevedo, Pedro A.

APPLICANT: Cahoon, Rebecca

APPLICANT: Cahoon, Rebecca

APPLICANT: Horrann, Refael

APPLICANT: Herrann, Billy Fred

APPLICANT: Herrann, Sefensin Polynucleotides and Methods of

TITLE OF INVENTION: Use

FILE REFERENCE: 35718/246703

CURRENT APPLICATION NUMBER: US/11/123,896

CURRENT APPLICATION NUMBER: 60/300,152

PRIOR APPLICATION NUMBER: 60/300,152

PRIOR APPLICATION NUMBER: 60/300,152

PRIOR APPLICATION NUMBER: 60/300,241

PRIOR PILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 469

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 59

LENGTH: 74

TYPE: PRT

ORGANISM: Glycine max

US-11-123-896-59
Search completed: March 28, 2006, 13:26:39 Job time: 1.984 secs
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US-11-123-896-59
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                                                                                                                                      5 GPSCLLLLTSEIDLPVKR 22
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7 FSCLILLELLIKVLLKNR 24
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                                                                                              GFLFLLLLVLASDVTVKR
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Ado25951 Human for
Adp24410 PRO pol/pp
Ads74158 Human LXA
Adx06659 Cyclin-de
Ady72333 Human for
Abu10712 Human G-p
Ady73573 Human G-p
Ady73573 Human FPR
Abb56354 Non-endog
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Ady73577 Human HGP
bu10072 Human HGP
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1316	1318	1318	1318	1318	1318	1318	1318	1318	1318	1321	1321	1325	1327	1327	1327	1327	1419	1419	1419	1420
72.4	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.7	72.7	72.9	73.0	73.0		73.0	78.1	78.1	78.1	78.2
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Ady73575 Humar	Ady73235 Humar	Adu01527 Human		Adp24713 PRC	•••	Adi53335 Human	Adh58988 Humar	Add32067 Human	Abp81729 Humar	Ads64571 Humar	Abg95161 Human		Adf70495 Orp	Ads64565 Human	Ads64561 Human	Abg95152 Human	Ado57848 Rat	Adi53331 Rat	Adh58984 Rat	Ado57850 Mouse
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## ALIGNMENTS

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RRESULT 1
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ID AAUT9
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XX Huma
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XX Huma
XX Homc
XX Chrc
XX Chrc
XX O7-P
PF 23-4
XX Home
XX Homc
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Weith A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-315580/35.
N-PSDB; ABK48101.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chronic obstructive pulmonary disease; COPD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human formyl peptide receptor like-1 receptor,
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The invention relates to determining an expression level of an ILM receptor (macrophage surface receptor), comprises determining the level of an ILM receptor expressed in a macrophage. Also included are a method of determining whether a substance is an activator or an inhibitor of an ILM receptor, involving applying the substance to a test system which generates a measurable read-out upon modulation of the ILM receptor or an ILM receptor function, a test system for determining whether a substance

Claim 7; Page 49-51; 79pp; English.

macrophage.

Determining an expression level of ILM (a macrophage surface receptor), for the diagnosis or monitoring of chronic inflammatory airway disease, comprises determining the level of the ILM receptor expressed in a

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is an activator or an inhibitor of an ILM receptor function, characterised in that the receptor is involved in a chronic inflammatory airway disease and where the receptor plays a role in mediating inflammation comprising: (i) an ILM receptor; (ii) an expression vector capable of expressing an ILM receptor in a cell; or (iii) a host cell transformed with an expression vector capable of expressing the ILM receptor and a substance determined to be an activator or inhibitor of an ILM receptor. The methods are useful for the diagnosis or monitoring of a cironic inflammatory disease, e.g. chronic bronchitis and chronic obstructive pulmonary disease (COPD). The substance determined to be an activator or inhibitor of an ILM receptor, is useful for treating the diseases and for modulating an ILM receptor in a macrophage. The present sequence is an ILM receptor which is differentially expressed and which is involved in causing the induction and/or maintenance of the hyperactive status of macrophages involved in an inflammatory process of the control of the status of macrophages involved in an inflammatory process of the hyperactive status of macrophages involved in an inflammatory process.
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Best Local S
Matches 351
                                                                                                                                                                                                                                                                                   gene
                                                                 08-OCT-2001; 2001GB-00024145
                                                                                                            02-OCT-2002; 2002WO-EP011034
                                                                                                                                                         17-APR-2003
                                                                                                                                                                                                  WO2003031650-A2
                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                   myocardial infarction; cardiant; antiarteri gene therapy; differential gene expression.
                                                                                                                                                                                                                                                                                                                           Cardiovascular disease; arteriosclerosis; ischaemia; angina
                                                                                                                                                                                                                                                                                                                                                                         Protein differentially expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                   10-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU89747;
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                        (FARB ) BAYER AG
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                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                         cardiovascular disease
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7.8e-196;
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밁 ঠ 밁 ঠ 문 5

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Predicting, diagnosing or prognosing a cardiovascular disease, angina, ischemia, myocardial infarction or arteriosclerosis by of a polynucleotide in a biological sample comprises detecting hybridization complex.
                                                                                                        Claim
                                                                                                                                                             N-PSDB;
                                                                                                                                                                                  Munnes M,
                                                                                                       3; Page 375-377; 454pp; English
                                                                                                                                                             ACA89920
                                                                                                                                                                                  Gehrmann
                                                                                                                                                                                  z,
                                                                                                                                                                                  Wick
                                                                                                                                                                                  Z
                                                                                                                                                                                  Schmitz
                                                                                                                                                                                  Q
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20

e.g. detection

Best Loca Matches Query Match Best Local The invention describes a method of predicting, diagnosing or prognosing a cardiovascular disease by detection of a polynucleotide in a biologic sample comprises hybridising at least one of the polynucleotide to a nucleic acid material of a biological sample, thus forming a hybridisation complex, and detecting the hybridisation complex. The polynucleotides, polypeptides, antisense molecule, antibody and reagent a polynucleotides, polypeptides, antisense molecule, antibody and reagent a polynucleotides, polypeptides, artisense molecule, antibody and reagent a polynucleotides, polypeptides, artisense molecule, antibody and reagent a polynucleotides, polypeptides, antisense molecule, antibody and reagent a polynucleotides, polypeptides, antisense molecule, antibody and reagent approach of treating a cardiovascular disease, e.g. arteriosclerosis, ischaemia, angina pectoris, or myocardial infarction. This sequence represents a protein identified in the invention a being differentially agreements a protein identified in the invention a being differentially agreements. Sequence 351 AA; differentially expressed in individuals with cardiovascular disease 301 301 241 181 181 121 241 121 351; 61 61 1 METNFSTPLNEYEEVSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVT Similarity LDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNF RVLTAVVASFFICWFFFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPM TICYLNLALADFSFTATLFFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIA LYVFVGQDFRERLIHSLPTSLERALSEDSAPTNDTAANSASPPAETELQAM 351 LYVFVGQDFRERLIHSLPTSLERALSEDSAPTNDTAANSASPPAETELQAM 351 RVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPM ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPL ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPL TICYLNLALADESETATLEELIVSMAMGEKWEEGWELCKLIHIVVDINLEGSVELIGEIA METNESTPLNEYEEVSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVT LDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNF Conservative 100.0%; 0 Score 1817; DB 6; Pred. No. 7.8e-196; ; Mismatches 0; Indels Length or prognosing in a biological 0, Gaps 180 120 300 180 120 300 240 60 60 240 0

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ABP81818 standard; protein; 351 ⋧

ABP81818;

04-MAR-2003 (first entry)

Human formyl peptide receptor-like receptor protein SEQ ID NO: 120.

RESULT 3
ABP81818
ID ABP8
XX
AC ABP8
XX
DT 04-)
XX
CKW G D
KW G D immunological-related cell proliferative disease; autoimmune disease; infaction; osteoarthritis; aller osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pa G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; cell regeneration-related disease; AIDS; c disease; allergy; cancer; pain;

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                                                                                                                                                                                                                                                Query Match
Best Local Sim
Matches 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating condition which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma; ulcer.
                                                                                                                                                                                                                                                                                                                       Sequence 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 1; 523pp;
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                                                                                                                                                                                                                                                                                                                                                          exemplification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-DEC-2001; 2001WO-US050107.
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                                                                                                                                                                                                                                                                                                                                                       proteins given in ABP81675 to ABP82018, plification of the present invention
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ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPL
                                                      LDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNF
                                                                                                      TICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIA
                                                                                                                                TICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIA
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Pred. No. 7.8e-196;
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           The invention relates to a method of screening for agents for treating formyl peptide receptor-like 1 (FPRLI)-related disorders in a mammal. The method involves detecting the binding of test compound to an FPRL1 polypeptide or polymucleotide, or determining the activity of an FPRL1 polypeptide at different concentrations of the test compound. FPRL1 is a grotein coupled receptor (GPCR) which is highly expressed in a variety of human tissues. It is expressed in varous brain tissues, cardiovascular system tissues, erythrocytes and other haemotological tissues, respiratory tissues, genito-unrological tissues such as prostate and placenta, and in various immune system tissues. In particular, it is expressed at a higher level in lungs affected with chronic obstructive pulmonary disease (COPD), compared with healthy lungs. The invention also encompasses a method of diagnosing an FPRL1-related disorder by quantification of FPRL1 polymucleotides, and pharmaceutical compositions for treating an FPRL1-related disorder. Therapeutic agents identified using the method of the invention can be used in the treatment of disorders such as haematological diseases, cardiovascular diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPCR; drug screening; diagnosis; haematological disease; cardiovascular disease, peripheral nervous system disease; central nervous system disease; respiratory disease; chronic obstructive pulmonary disease; COPD; asthma; genito-urological disease; inflammatory disease; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                             Screening for therapeutic agents for treating a disease e.g., cardiovascular, inflammatory, or respiratory diseases by contacting a test compound with a FPRL1 polypeptide or polynucleotide and detecting binding of the test compound.
                                                                                                                                                                                                                                                                                                                                                           Disclosure;
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lrug screening; diagnosis; haematological disease;
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                                                                                                                                                            14-JUN-2002; 2002JP-00173798.
15-JUL-2002; 2002JP-00205470.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (e.g., COPD), asthma, genito-urological diseases, or inflammatory diseases. The present sequence represents human FPRL1 protein.
                          regulation and treatment
                                                    Screening
                                                                                                                                                                                                   12-JUN-2003; 2003WO-JP007500
                                                                                                                                                                                                                             24-DEC-2003.
                                                                                                                                                                                                                                                       WO2003106683-A1
                                                                                                                                                                                                                                                                                 Homo
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                                                                                                                                  (TAKE ) TAKEDA CHEM IND LTD.
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                        ng potential humanin receptor agonists and antagonists using and G-coupled receptor protein FPRL1 or FPRL2 for apoptosis ion and treatment and prevention of disorders of nerve and b
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Pred. No. 7.8e-196;
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Best Local Simi
Matches 351;
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                                                                                                  RVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPM
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100.0%; Pred. No. 7.8e-196;
tive 0; Mismatches 0;
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RESULT 6
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humanin-like peptide receptor protein; G-protein coupled receptor; FPRL1;
FPRL2; transmembrane G-protein coupled receptor; nervous system disorder;
Alzheimer's disease; Parkinson's disease; Down's syndrome;
Huntligton's disease; muscular dystroph; prion disease;
Creutzfeldt-Jacob disease; diabetic neuropathy; multiple sclerosis;
cerebral ischaemia; apoplexy; brain haemorrhage;
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WO2004008141-A1

Homo

sapiens.

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RESULT 7
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Screening compounds modifying binding of humanin-like peptide to its receptor protein for identification of apoptosis regulators and remedies for nervous system disorders, e.g. Alzheimer's disease.
G protein-coupled receptor; GPCR; drug screening; diagnosis; transgenic mouse; neurological disorder; adrenal gland disorder;
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                                                   Human GPCR FPRL1, SEQ ID NO:793.
                                                                                     29-JUL-2004
                                                                                                                       ADO29691;
                                                                                                                                                       ADO29691 standard; protein; 351 AA
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colon disorder; intestinal disorder; cardiovascular disorder; muscular disorder; blood disorder; intunne disorder; bone disorder; joint disorder; blood disorder; nutritive disorder; bone disorder; kidney disorder; liver disorder; nutritive disorder; cancer; kidney disorder; liver disorder; lung disorder; breast disorder; ovary disorder; uterus disorder; prostate disorder; testis disorder; skin disorder; stomach disorder; prostate disorder; spleen disorder; thymus disorder; stomach disorder; antiparkinsonian; antimanic; cytostatic; antiinflammatory; vasotropic; antidiarrhoeic; antidiabetic; cytostatic; antiinflammatory; vasotropic; antidiarrhoeic; antidiabetic; virucide; hepatotropic; antibacterial; antidiarrhoeic; antideborrhoeic; dermatological; antiulcer; antithyroid; antiallergic; anorectic; immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human; receptor.
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Homo sapiens.

WO2004040000-A2.

13-MAY-2004

09-SEP-2003; 2003WO-US028226

09-SEP-2002; 2002US-0409303P. 09-APR-2003; 2003US-0461329P.

(PRIM-) PRIMAL INC

Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F; Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D, Zeng H;

WPI; 2004-390329/36.

Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina pectoris, Parkinson's disease.

Claim 151; SEQ ID NO 793; 542pp; English

The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to CC sequences at least 98 identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic CC compounds useful in the transgene or in an endogenous GPCR gene; cells derived comprising a GPCR gene of the invention; a mouse comprising a transgenic mite; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising probes which hybridise to GPCR polymuclectides of the invention. The invention further discloses variants of the GPCR polymeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, calarnoea, food poisoning or irritable bowell compression, diabetic neuropathy, parkinson's disease or schizophrenia); disorders of the colon or intestine (e.g., Crohn's disease, diarnoea; food poisoning or irritable bowell syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or myocardial infarction); muscular disorders (e.g., autoimune disorders (e.g., antended or leukaemia); immune disorders (e.g., autoimune disorders (e.g., obesity, enzyme deficiency-related diseases or vitamin deficiency-related corrects, but a town of the protect (e.g., cancers). The present sequence represents a GPCR of the colonic format directly from WIPO at the printed specification; those sequences not shown were obtained in celectronic format directly from WIPO at

equence 351 AA;

100.0%;

Score 1817; DB 8; Pred. No. 7.8e-196;

Length 351;

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Best Local Similarity
Matches 351; Conserv
The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
                                                                                                                        Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of
                                                                                                                                                                                                           Wohlgemuth J, Rosenberg S;
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20-DEC-2002; 2002US-00325899.
                                                                                    Claim 65;
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RESULT 9
AD057846
ID AD057846
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XX Huma
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XX W020
XX W021-W
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PR 06-W
XX 07-W
PR 18-W
PR 03-W
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Best Local Similarity
Matches 351; Conserv
              Hinuma S,
Nishi K;
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                                                                                        07-NOV-2002; 2002JF-00324189.

18-DEC-2002; 2002JF-00367119.

05-NAR-2003; 2003JF-00059073.

03-JUL-2003; 2003JF-00191359.
                                                                                                                                                                                                                                                                                      neuroprotective; antianginal; cerebroprotective; antianaemic; virucide; antiinfective; immunomodulator; asthma; allergic disease; inflammation; arteriosclerosis; FPRL1; formyl peptide receptor-like 1; human.
                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                       antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                   Human formyl peptide receptor-like 1 SEQ
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                                                            (TAKE ) TAKEDA
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                              Kobayashi M,
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Pred. No. 7.8e-196;
Mismatches 0;
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                                 Okubo
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RESULT 10
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Best Local S
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                 PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
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                                                                                            PRO polypeptide
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                                                                                            ID NO:1588
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Pred. No. 7.8e-196;
Mismatches 0;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   graft-versus-host disease. The present sequence represents a PRO protein
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DB; ADP24409.
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                                                                                                                                                                                                                                                                                                                     Score 1817; DB 8;
Pred. No. 7.8e-196;
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RESULT 11
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   Query Match
Best Local S
Matches 351
                                                                                                                                                                                                              The present sequence is that of the human LXA4 receptor (ALX), a G-
protein coupled receptor (GPC). The invention is based, in part, on the
recognition that resolvin El receptor (Reso ERI) shares similar
structural features to LO-derived eicosanoid receptors such as the LXA4
receptor. A claimed method of identifying a receptor that mediates an
antinflammatory activity of a resolvin substance comprises: introducing a
nucleic acid configured to express a GPCR into a cell that does not
endogenously produce the GPCR; contacting the cell with a substance
comprising a resolvin; and detecting that the cell has a reduced cytokine
induced activation of a NF-kB transcription factor relative to a cell not
contacted by the substance. A claimed method for screening a candidate
substance for antiinflammatory activity comprises detecting that the
candidate substance alters an activity mediated by a GPCR. The GPCR
preferably has sequence identity within the second intracellular loop or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening candidate substance for anti-inflammatory activity, involves contacting cell expressing Reso E receptor with candidate substance, and detecting biological activity mediated by Reso E receptor.
                                                                                                                             Sequence 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 3; 33pp; English.
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      Local Similarity
hes 351; Conser
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100.0%; Score 1817; DB 8;
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cive 0; Mismatches 0;
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                                                                                                                                                                                              of human ALX.
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                                                                Length 351;
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Biomarkers useful for predicting to a cancer treatment comprising dependent kinase activity. or determining administration of a modulator f a mammal of cyclin-

Claim 5; SEQ ID NO 1424; 141pp; English

This invention describes a novel method of predicting or determining whether a mammal will respond or is responding to an anti-cancer agent that modulates cyclin-dependent kinase (cdk) activity. The method comprises measuring the level of one or more biomarkers selected from 2774 biomarkers given in the specification (nucleotide sequence SEQ ID NO:1246 (Genbank EST W28729) is especially preferred). The method of the invention is utilized in a kit for determining or predicting whether patient would be susceptible or resistant to treatment by an agent modulating cdk activity. The invention also describes a method for utilizing individualized genetic profiles for treating diseases and disorders based on patient's response and molecular level, specialized microarrays comprising the biomarkers described, antibodies directed

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Gaps

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Best Local Simi
Matches 351;
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Identifying compound that changes amyloid beta precursor protein processing in cell, involves exposing cell to compound, comparing activity level of polypeptide before and after exposing cell to compound the compound of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuroprotective; nootropic; gene therapy; substrate inhibition; gene expression; diagnosis; Alzheimers disease; neuroprotective; nootropic; degeneration; neurological disease; cognitive disorder;
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Pred. No. 7.8e-196;
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CC changes the amyloid-beta precursor processing in a cell,
CC involving providing a host cell expressing a polypeptide having one of 14
CC amino acid sequences (SEQ ID No. 15-28), determining activity level of
CC polypeptide, exposing the host cell to a compound, determining activity
CC level of the polypeptide, and identifying the compound, by which the
CC second activity level is less than the first activity level. Also
CC described are: changing the amyloid-beta precursor protein processing of
CC or cell; a polynucleotide (I) comprising a nucleotide sequence chosen from
CC one of 310 fully defined 21 base pair sequences (SEQ ID No. 29-338) given
CC in the specification; a vector (II) comprising (I); and diagnosing a
CC pathological condition involving cognitive impairment or a susceptibility
CC to the condition in a subject. (MI) is useful for identifying a compound
CC to the condition in a subject. (MI) is useful for identifying a compound
CC or (II) is useful as a medicament or for producing medicament for
CC impairment. This is the amino acid sequence of human receptor FPRL1
CC impairment. This is the amino acid sequence of human receptor FPRL1
CC inhibition of amyloid beta production. Note: The invention claims SEQ ID
CC NO's 1-28 which are not shown in the specification.
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Sequence 351 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  identifying compound
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Length

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RESULT 14
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musculoskeletal disease; antiarthritic; antirheumatic; Alzheimers disease; neurological disease; degeneration; nootropic; neuroprotective; asthma; antiasthmatic; respiratory disease; trauma; vulnerary; injury; radiation injuries; antiemetic; cytostatic; renal disease; nephrotropic; endocrine disease; genitourinary disease;
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CC relates to the use of the FPRLI as a tool to identify compounds affective (C compounds as therapeutics.) A method of screening for a compound able to (C compounds as therapeutics.) A method of screening for a compound able to (C contracting a recombinant cell with a test compound, where the recombinant (C coll comprises a recombinant nucleic acid expressing FPRLI (provided the CC call does not have endogenous FPRLI expression); and (b) determining the C call does not have endogenous FPRLI expression; and (b) determining the C call tool of the test compound to affect one or more activities of FPRLI. A CC compound that activates a FPRLI receptor subtype is used in a claimed (C amputation, cancer, bacterial infection, irritable bowl syndrome, CC amputation, cancer, bacterial infection, physical inflammation of physical trauma and radiation exposure, vasoconstriction as a result of respiratory distress syndrome, (Crohn's disease, endotoxin shock, renal disease, benign prostatic hypertrophy, myocardial ischemia, (C glomerular disease, benign prostatic hypertrophy, myocardial ischemia, (C renal disease, cardiovascular disease and hypertension or chemical injury (all claimed). Also claimed are: cells that express FPRLI receptor, which are used in a claimed method of identifying agonists of FPRLI, a method (C is associated with rheumatoid arthritis, Alzheimer's disease or asthma, (C resultes from physical inflammation, where the inflammatory response results from CC sacutive coxygen species to evoke vascular leakage or edema, (is associated with rheumatoid arthritis, Alzheimer's disease or asthma, (c results from physical inflammation to treat or prevent a cincluding slomerular disease, a cardiovascular disease, including slomerular disease, a cardiovascular disease including corrective response or condition such as renal hemodynamic disease, including alomerular disease, a cardiovascular disease including the provided the condition such as suffidopeptide condition and a method of inducing vasodilation to treat or p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glomerular disease; cardiovascular disease; hypertension; hypotensive; myocardial infarction; cardiant; myocardial ischemia; vasotropic; allergy; antiallergic; immune disease; shock; gout; antigout; musculoskeletal disease; psoriasis; antipsoriatic; dermatological disease; psoriasis; antipsoriatic; respiratory distress syndrome; respiratory-gen; respiratory disease; crohns disease; gastrointestinal-gen; gastrointestinal disease; crohns disease; gastrointestinal-gen; gastrointestinal disease; benign prostatic hypertrophy; neoplasm; inflammatory bowel disease; benign prostatic hypertrophy; neoplasm; inflammatory bowel disease; brain injury; cerebroprotective; systemic lupus erythematosus; brain injury; vasoconstriction; pain; analgesic; diabetes; antidiabetic, bartorial inforticit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nash N,
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10-NOV-2003; 2003US-0519085P.
30-JUL-2004; 2004US-0592926P.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; receptor; G-protein coupled receptor; HGPRBMY39; cancer; male reproductive disorder; testicular disorder; immune disorder; inflammatory disorder; testicular disorder; leukaemia; bone marrow disorder; testicular cancer; proliferative disorder;
                           WPI; 2003-313245/30
                                                                                Ramanathan CS,
                                                                                                                                                                                    07-SEP-2001;
27-NOV-2001;
                                                                                                                                                                                                                                                                    06-SEP-2002; 2002WO-US028582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU10071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leukotriene in a subject, where the response is a renal vasoconstrictive response including mild vasoconstriction such as chronic renal disease and chronic severe vasoconstriction such as glomerular kidney disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU10071 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 351 AA;
                                                                                                                                  (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         leural disorder; Alzheimer's disease; prion disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301
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2001US-0333658P
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                                                                             Gopal
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2. .370
                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "This region is claimed in claim
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Pred. No. 7.8e~196;
; Mismatches 0;
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                                                                                   Feder
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related to aberrant G-protein coupled signalling, particularly N-formyl peptide receptor dependent signalling; a disorder related to aberrant G-protein coupled receptor dependent phosphatidylinositol-calcium signalling; a disorder related to aberrant G-protein couple receptor dependent phosphatidylinositol or calcium second messenger activation; an immune disorder an inflammatory disorder; a developmental disorder; a disorder that would benefit from inhibition of a leukotriene B4-dependent proinflammatory signal, aberrant N-formyl peptide signalling; aberrant neutrophil activation; a disorder associated with byper neutrophil activation; a disorder associated with below normal neutrophil activation; a disorder associated with below normal neutrophilater activation.
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protein coupled receptor HGPRBMY39 (or its fragment domain or epitope),
its complement or a polynucleotide capable of hybridising under stringent
conditions to it. Also included are a HGPRBMY39 recombinant vector, a
recombinant host cell comprising the vector sequences (used to express
and make the protein), an isolated HGPRBMY39 polypeptide, and an anti-
HGPRBMY39 antibody. The HGPRBMY39 polynucleotides and polypeptide is
useful for preventing, treating or ameliorating e.g. a (male)
reproductive disorder; a testicular disorder or cancer; a disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oxidation states; a disorder related to aberrant superoxide generation; leukaemia; a bone marrow disorder; cancer; proliferative disorders; neural disorders a disorder related to aberrant neutrophil chemotaxis; Alzheimer's disease; prion disorders; and a bone metabolism disorder. The provider of the content of the conte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human G-protein coupled receptor, HGPRBMY39, useful for treating or preventing e.g. immune, inflammatory, developmental, proliferative, neural, reproductive, bone marrow or prion disorders.
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Pred. No. 8.4e-196;
Mismatches 0; Indels 0
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Search completed: March 28, 2006, 13:14:57 Job time : 254.22 secs

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88.3	88.3	88.3	88.3	88.3	92.5	92.5	92.5	92.5	92.5	92.5	95.0	95.8	96.7	96.7	96.7	96.7	96.7	96.7	97.5	97.5
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Aab81876 N	Aab81886 N	Aab81879 N	Ad153327 H	_	Adf95069 H		<b>Аао30329 Н</b>	Aab81839 N	Aab73996 H	Aab81842 N	Aab81837 N	Aab81841 N	Adf95070 H	Adi53326 H	Adh58978 H	Adf95053 H	Aab81838 N	Aab73995 H	Adf95066 H	Adf95063 H
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# ALIGNMENTS

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                                   The present sequence is provided in a specification relating to a method for screening for disease inhibiting genes and peptides. Nucleic acids originating in cells from patients suffering from the disease are introduced into a host cell and expressed in that cell, the effect on cell death is determined, and nucleic acids are selected in which a depressant effect on cell death is observed. The method is useful in the identification of drugs for treatment and gene therapy of cell-death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; disease inhibiting gene; gene screening; protein s drug identification; gene therapy; cell-death associated central nervous system disorder; Alzheimer's disease; Huntington's disease; cerebrospinal ataxia; apoptosis; familial amyotrophic lateral sclerosis; HN.
                                                                                                                                                                                                                                                                                                                                                                                                                     Screening for disease inhibiting genes and peptides nervous system diseases involving cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-257984/26.
N-PSDB; AAF82222.
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29-JUN-2000; 2000JP-00201456.
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VAB81836

associated diseases of the central

nervous system,

such as

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AC ABB4
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Matches 24
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         07-FEB-2002
                                                     ABB44628;
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanin peptides which inhibits cell death useful for treatment Alzheimer's and other nervous system diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nishimoto
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                                                                                               ABB44628 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 94; 116pp; Japanese.
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29-JUN-2000; 2000JP-00201456.
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of new drugs useful
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The present invention relates to protective sequence proteins (ABB44624-ABB44330) and their coding sequences (ABA82701-ABA82937). The sequences, when introduced into a cell either predisposed to undergo cell death or in the process of undergoing cell death, prevent, delay or rescue the cell from death, hence, these sequences are named "protective sequences".
                           The sequences are useful for treating and/or ameliorating cancer, autoimmune diseases and neurological disorders e.g. stroke. Furth examples of diseases which may be treated by the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                      New protective sequences and their products, useful for diagnosing and treating diseases involving cell death, including neurological disorders e.g. stroke and for identifying modulators of expression of the
given in the specification
                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 4; 283pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; protective sequence; cell death; cancer; autoimmune disease; neurological disorder; stroke; cytostatic; neuroprotective; gene th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human
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                                     invention
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                                     Best Loc
Matches
                                                        Query Match
                                              Local
                                               Similarity
          MAPRGFSCLLLLTSEIDLPVKRRA 24
MAPRGFSCLLLLTSEIDLPVKRRA 24
                                    100.0%;
ilarity 100.0%;
Conservative 0;
                                      0
                                    Score 120; DB 5;
Pred. No. 1.3e-12;
Mismatches 0;
                                                       Length 24;
                                     Indels
                                      0,
                                      Gaps
                                      0
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Sequence 24

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AAU73274;
               AAU73274 standard;
               peptide;
               24
               ₹
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Human protective DNA sequence CNI-00736 open reading frame #5.

12-MAR-2002

(first

entry)

RESULT 4
AAU73274
ID AAU7
XX AAU7
XX AAU7
XX AAU7
XX Huma
XX Huma
XX Huma
KW isch
KW cere
KW meta
KW diak
KW nutx
KW diak
KW nutx
XX CNIXX Homc
XX WO21
XX WO21 Human; protective sequence; cell death; central nervous system; stroke; ischaemia; open reading frame; ORF; cerebral herniation; septic embolist cerebral oedema; meningitis; protozoal infection; malaria; CNI-00733; metazoal infection; vascular disease; eye; macular degeneration; trauma diabetic retinopathy; epidural haematoma; tumour; degenerative disease; nutritional condition; environmental condition; metabolic condition; Homo sapiens. CNI-00736; CNI-00738; CNI-00742; CNI-00748; cancer; gene therapy embolism;

01-NOV-2001

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RRSULT 5
AAU69614
ID AAU6
XX AAU6
XX AAU6
XX AAU6
XX AAU6
XX Cell
XX Cell
XX Huma
XW menti
XW menti
XW moto
XW moto
XW orall
XW orall
XW oral
XW boly
XW ooste
XW ooste
XX Homo
XX Homo
XX Homo
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosing a protective sequence-mediated condition, disorder or disease in an individual. The treatable disorders are preferably of the central nervous system of humans including ischaemia-related conditions such as stroke, cerebral herniation, septic embolism, cerebral oedema, infections such as machasia, metazoal such as meningitis, protozoal infections such as malaria, metazoal infections such as echinococcosis, vascular diseases such as ischaemic encephalopathy, conditions involving the eye such as macular degeneration, diabetic retinopathy, trauma such as epidural haematoma, tumours such as primary intracranial tumours, degenerative diseases such as Alzheimer's disease and nutritional, environmental and metabolic conditions. Sequences AAU73255-AAU7378 tropresent open reading frames of the human protective sequences of the business of the such as protective sequences aautomatic trauma such as protective sequences aautomatic protections.
                                                                           diabetic neuropathy; autoimmune haemolytic anaemia; respiratory system; oral cavity; gastrointestinal tract; liver, cirrhosis; pancreatitis; polycystic renal disease; urinary tract; genitalia; endometriosis; breast; chronic mastitis; thyroid gland; Hashimoto's thyroiditis; adrenal gland; skin; psorissis; muscular atrophy; bone marrow;
                                                                                                                                                                               Human; protective sequence; cell death; cerebral oedema; infection; meningitis; degenerative disease; Alzheimer's disease; heart disease; motor neuron disease; demyelinating disease; multiple sclerosis; asthma; nutritional condition; peripheral nervous system disorder; ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     introduced into a cell either predisposed to undergo cell death or in the process of undergoing cell death, prevent, delay, or rescue the cell from death, relative to a corresponding cell into which exogenous nucleic acids have been introduced. The sequences of the invention are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polypeptides and polynucleotides comprising protective sequences useful for preventing, delaying or rescuing a cell from death in disease, condition or disorders such as Alzheimer's disease, stroke, tumors,
                                                                                                                                                                                                                                                                                                                                     30-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                              AAU69614;
                                                                                                                                                                                                                                                                                                                                                                                                                     AAU69614 standard; protein; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 17; Fig 5F; 228pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-066433/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence, which is a polynucleotide comprising sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAPRGFSCLLLLTSEIDLPVKRRA 24
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                                                                                                                                                                                                                                                                                         protective sequence CNI-00725, protein #4.
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                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                              cancer;
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Pred. No. 1.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polynucleotides
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The invention relates to isolated protective sequence polypeptides (I) and polynucleotides (II). (II) is useful for transferring a protective sequence into a cell, which delays and/or prevents the cell from undergoing cell death. Protective sequences, their products or antibodies are useful diagnostically, prophylactically, therapeutically or as targets for treatment and diagnosis of conditions, disorders or diseases involving cell death. The protective sequences and their products are useful for preventing or treating disorders of the central nervous system including neurological and psychiatric conditions, cerebral oedema, infections such as meningitis, degenerative diseases such as Alzheimer's and motor neuron disease, demyelinating diseases such as multiple sclerosis, nutritional conditions, disorders of the peripheral nervous system including diabetic neuropathy, disorders which cause cell death in organ systems including blood vessels, heart (ischaemia), blood cells
                                                                                                                                       (autoimmune haemolytic anaemia), respiratory system (asthma), oral cavity, gastrointestinal tract, liver (cirrhosis), pancreatitis, polycystic renal disease, urinary tract, genitalia (congenital anomalies), endometriosis, breast (chronic mastitis), thyroid gland (Hashimoto's thyroiditis), adrenal gland, skin (psoriasis), musculoskeletal system (muscular atrophy), bone marrow or bone (osteoporosis). The compositions promote cell death and are useful for treating and/or ameliorating cancer and autoimmune diseases. The caused by infection which induce cell death. (I) is useful to raise an
                                                        immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as markers for tissues in which the corresponding protein is expressed and to isolate receptors or ligands. AAU69571-AAU69736 represent the protective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids referred as protective sequences products for diagnosing, treating diseases involving including neurological disorders e.g. stroke and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; Fig
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                                         sequences as
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                                           described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INC
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                                           invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and their encoded cell death, identifying
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Sequence 24

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                                             Best
                                    Matches
                                                      Query Match
                                              Local
        1 MAPRGESCLLLLTSBIDLPVKRRA 24
                                   Similarity
24; Conserv
MAPRGFSCLLLLTSEIDLPVKRRA 24
                                  100.
nilarity 100.
Conservative
                                            . 08 ;
                                   0
                                           Score 120; DB 5;
Pred. No. 1.3e-12;
                                   Mismatches
                                                      Length 24
                                    Indels
                                   0,
                                   Gaps
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0

RESULT 6
AAO30161
ID AAO3
XX
AC AAO3
XX
DT 03-S
XX
DB Huma AAO30161 standard; peptide; 24

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03-SEP-2003 (first entry)

Human humanin protein, HN1

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RESULT 7
AAO30314
ID AAO3
XX
AC AAO3
XX
DT 22-6
XX
Hume
XX
Hum
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanin; bax; bid; therapy; Alzheimer's disease; Parkinson's disease; neuron cell death; cancer; autoimmune disorder; nootropic; vasotropic; anticonvulsant; tranquilliser; vulnerary; cardiant; antiinflammatory; stroke; Huntington's disease; trauma; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method for screening genes involved in aging and/or aging-associated diseases (AAD) or in oxidative stress. The method involves mutating and cultivating a yeast cell, enriching the population for mother cells, labelling the mother cells and isolating the highly labelled cells. The present sequence is human humanin protein, HNI. This sequence is used to illustrate the method of the invention
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                        Reed JC,
                                                                                                                                        28-NOV-2001; 2001US-0334149P
                                                                                                                                                                                                   27-NOV-2002; 2002WO-US038191.
                                                                                                                                                                                                                                                              05-JUN-2003.
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                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                (BURN-) BURNHAM INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2003-505183/47.
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100.0%; Pred. No. 1.3e-12;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             that modulates the binding of humanin to bax and/or bld. The method is useful for diagnosing and/or treating disorders associated with the humanin-bax or humanin-bid complex, such as Alzheimer's disease, stroke Parkinson's disease, Huntington's disease, trauma, amyotrophic lateral sclerosis, neuron cell death, cancer or inflammatory or autoimmune disorders. The present sequence is human humanin (cytosolic form) peptide. This sequence is used to illustrate the method of the invention
                                                                          New Humanin derivative that protects a neuronal cell from cytotoxicity, useful for treating neurodegenerative disorders (e.g. Alzheimer's disease), comprises a D-amino acid (e.g. D-Serine) or a phosphorylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying modulators of apoptosis, in particular binding modulators of humanin to bax or bid, useful for diagnosing and/or treating disorders such as Alzheimer's disease, Parkinson's disease, cancer and inflammatory
                                                                                                                                            WPI; 2004-061983/06.
                                                                                                                                                                           Nishimoto
                                                                                                                                                                                                                                                                     16-MAY-2003; 2003WO-JP006139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanin peptide derivative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to method for identifying an effective compound that modulates the binding of humanin to bax and/or bid. The method is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 3B; 141pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAPRGFSCLLLLTSBIDLPVKRRA 24
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Pred. No. 1.3e-12;
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                                                                                                           The invention relates to a derivative of humanin (HN) that protects a neuronal cell from cytotoxicity, where the derivative contains at least one D-amino acid or phosphorylated amino acid, or where the derivative has an addition of one or more amino acids having an activity of forming a multimer. The humanin derivatives are useful in protecting neuronal cells from cytotoxicity related to neurodegenerative diseases. The composition and method are useful in treating neurodegenerative diseases. Albeimer's disease. The present sequence represents an activities of the present sequence represents and the present sequence represents an activity of the present sequence and the present sequence activity of the present sequence activity of the present sequence and the present sequence activity of the present sequence 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Humanin derivative that protects a neuronal cell from cytotoxicity, useful for treating neurodegenerative disorders (e.g. Alzheimer's disease), comprises a D-amino acid (e.g. D-Serine) or a phosphorylated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nishimoto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003097687-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; SEQ ID NO 8;
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..3e-12;
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Sequence 24

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MAPRGESCLLLLISEIDLPVKRRA 24

MAPRGFSCLLLITSEIDLPVKRRA 24

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RESULT 10
ADP95060
ID ADP95060
ADP95060
ADP95060
AC ADP95
XX ADP95
XX ADP95
XX Human
XX Hu, h
KW HN, h
KW Alzhe
XX Synth
OS Homo
XX Key
FH Key
FH Misc-
FT M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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                          Query Match
Best Local S
     Matches
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Best Local
                                                                                                                                                                                           neuronal cell from cytotoxicity, where the derivative contains at least one D-amino acid or phosphorylated amino acid, or where the derivative has an addition of one or more emino acids having an activity of forming a multimer. The humanin derivatives are useful in protecting neuronal cells from cytotoxicity related to neurodegenerative diseases. The composition and method are useful in treating neurodegenerative diseases.
                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Humanin derivative that protects a neuronal cell from cytotoxicity, useful for treating neurodegenerative disorders (e.g. Alzheimer's disease), comprises a D-amino acid (e.g. D-Serine) or a phosphorylated
                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a derivative of humanin (HN) that protects
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; SEQ ID NO 9; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-061983/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAY-2003; 2003WO-JP006139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADF95060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003097687-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HN; humanin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADF95060 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                 peptide
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                            Similarity
                                                                                                             24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAPRGFSCLLLLTSEIDLPVKRRA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAPRGFSCLLLLTSEIDLPVKRRA 24
                                                                                                                                                                    such as Alz
derivative.
                                                                                                             ₽,
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     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytotoxicity; neuroprotective; nootropic; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "D-form residue"
                            100.0%; Score 120; DB 8 100.0%; Pred. No. 1.3e-1
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     Mismatches
                                                         8
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                                                      Length
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                                                            24;
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     0
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Gaps
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  0
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RESULT 12
ADF95057
ID ADF95
XX
AC ADF95
XX
PT 26-FF
XX
DE Human
XX
DKW HN;
KW HN;
KW Alzh
XX
OS Synt
OS Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
ADF95052
ID ADF95
XX ADF95
XX ADF95
XX ADF95
XX HUMAN
XX HUMAN
XX HOMO
PM WO200
XX HOMO
PM WO210
XX HOMO
PM WO210
PM WO210
PM WO210
PM WO210
PM WO210
PM WO210
PM WP1;
DR N-PSI
XX N18hi
X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a derivative of humanin (HN) that protects a neuronal cell from cytotoxicity, where the derivative contains at least one D-amino acid or phosphorylated amino acid, or where the derivative has an addition of one or more amino acids having an activity of forming a multimer. The humanin derivatives are useful in protecting neuronal cells from cytotoxicity related to neurodegenerative diseases. The composition and method are useful in treating neurodegenerative diseases, such as Alzheimer's disease. The present sequence represents a HN wild-type peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Humanin derivative that protects a neuronal cell from cytotoxicity, useful for treating neurodegenerative disorders (e.g. Alzheimer's disease), comprises a D-amino acid (e.g. D-Serine) or a phosphorylated
                                                                                                                                                                              Humanin peptide
                                                                                                                                                                                                                                            26-FEB-2004
                                           Synthetic
                                                                                                   Alzheimer's
                                                                                                                             HN; humanin; cytotoxicity; neuroprotective; nootropic; gene therapy;
                                                                                                                                                                                                                                                                                                   ADF95057
                                                                                                                                                                                                                                                                                                                                                       ADF95057 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; SEQ ID NO 1; 82pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nishimoto I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAY-2002; 2002US-0380958P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HN; humanin; cytotoxicity; neuroprotective; nootropic; gene therapy;
Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Humanin (HN) wild-type peptide sequence
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                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-MAY-2003; 2003WO-JP006139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (/HSIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2004-061983/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAPRGFSCLLLLTSEIDLPVKRRA 24
                                                                                                   disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                         (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                    derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                    P-S7/14 HN
                                                                                                                                                                                                                                                                                                                                                          24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 120; DB 8;
Pred. No. 1.3e-12;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                          ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₿
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ADF95056
ID ADF95
XX ADF95
XX ADF95
XX ADF95
XX Human
XX Human
XX HX; h
KW Alzhe
XX Synth
OS Synth
OS Homo
XX Hoy
FH Key
FT Modif
FT
XX WO20(
XX X
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                           neuronal cell from cytotoxicity, where the derivative contains at least one D-amino acid or phosphorylated amino acid, or where the derivative has an addition of one or more amino acids having an activity of forming a multimer. The humanin derivatives are useful in protecting neuronal cells from cytotoxicity related to neurodegenerative diseases. The composition and method are useful in treating neurodegenerative disorders, such as Alzheimer's disease. The present sequence represents a HN peptide derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Humanin derivative that protects a neuronal cell from cytotoxicity, useful for treating neurodegenerative disorders (e.g. Alzheimer's disease), comprises a D-amino acid (e.g. D-Serine) or a phosphorylated
                                                                                                                         Synthetic
                                                                                                                                                            HN; humanin; cytotoxicity;
                                                                                                                                                                                   Humanin peptide derivative
                                                                                                                                                                                                            26-FEB-2004
                                                                                                                                                                                                                                     ADF95056;
                                                                                                                                                                                                                                                            ADF95056 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a derivative of humanin (HN) that protects a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-061983/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAY-2002; 2002US-0380958P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Modified-site
                                     WO2003097687-A2
                                                                                                                                                Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAY-2003; 2003WO-JP006139
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                                                                        Modified-site
                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NISH/) NISHIMOTO I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acid.
                                                                                                                                                                                                                                                                                                                                      1 MAPRGFSCLLLLTSEIDLPVKRRA 24
                                                                                                                                                                                                                                                                                                                                                                       24;
                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                         MAPRGFSCLLLLTSBIDLPVKRRA 24
                                                                                                                                                 disease.
                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "phosphorylated"
14
                                                          /note= "phosphorylated"
                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                         peptide;
                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; 82pp; English
                                                                                                                                                                                     P-87
                                                                                                                                                            neuroprotective; nootropic; gene therapy;
                                                                                                                                                                                                                                                             24
                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                 Score 120; DB 8
Pred. No. 1.3e-1
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                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 8
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                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                          Indels
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27-NOV-2003

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neuronal cell from cytotoxicity, where the derivative contains at least one D-amino acid or phosphorylated amino acid, or where the derivative has an addition of one or more amino acids having an activity of forming a multimer. The humanin derivatives are useful in protecting neuronal cells from cytotoxicity related to neurodegenerative diseases. The composition and method are useful in treating neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Humanin derivative that protects a neuronal cell from cytotoxicity, useful for treating neurodegenerative disorders (e.g. Alzheimer's disease), comprises a D-amino acid (e.g. D-Serine) or a phosphorylated amino acid.
                     New Humanin derivative that protects a neuronal cell from cytotoxicity, useful for treating neurodegenerative disorders (e.g. Alzheimer's comprises a D-amino acid (e.g. D-Serine) or a phosphorylated
             disease), comprises amino acid.
                                                                            WPI; 2004-061983/06.
N-PSDB; ADF95077.
                                                                                                                                                                                             16-MAY-2003; 2003WO-JP006139
                                                                                                                                                                                                                                               WO2003097687-A2
                                                                                                                                                                                                                                                                                                 HN; humanin; Alzheimer's
                                                                                                                                                                                                                                                                                                                                        Humanin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a derivative of humanin (HN) that protects a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; SEQ ID NO 5; 82pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nishimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAY-2002; 2002US-0380958P
                                                                                                                 Nighimoto
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                                                                                                                                                                                                                      27-NOV-2003.
                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                           ADF95078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HN peptide derivative.
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                                                                                                                                           (NISH/) NISHIMOTO
                                                                                                                                                                                                                                                                                                                                                                                                                   ADF95078 standard; peptide; 24 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            such as Alzheimer's disease.
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                                                                                                                                                                                                                                                                                                                                       wild-type peptide sequence.
                                                                                                                                                                                                                                                                                                             cytotoxicity; neuroprotective; nootropic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2003WO-JP006139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 120; DB 8;
Pred. No. 1.3e-12;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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disorders, HN peptide

such as Alz derivative.

as Alzheimer's

disease.

present sequence represents

The invention relates to a derivative of humanin (HN) that protects a neuronal cell from cytotoxicity, where the derivative contains at least one p-amino acid or phosphorylated amino acid, or where the derivative has an addition of one or more amino acids having an activity of forming a multimer. The humanin derivatives are useful in protecting neuronal cells from cytotoxicity related to neurodegenerative diseases. The composition and method are useful in treating neurodegenerative

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RESULT 15
ADF95058
ID 95058
ID 95058
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                                                                                                                                                                                                                                                                                                                                                  disease), c
amino acid.
                                                                                                                                                                                                                                                                                                                                                                       New Humanin derivative that protects a neuronal cell from cytotoxicity, useful for treating neurodegenerative disorders (e.g. Alzheimer's disease), comprises a D-amino acid (e.g. D-Serine) or a phosphorylated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADF95058 standard; peptide;
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                                                                                                                                                                                                                                                                                         Claim 8; SEQ ID NO 7; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-MAY-2003; 2003WO-JP006139
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100.0%; Pred. No. 1.3e-12;
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seq length: 2000000000
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                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
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120
PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
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                                                                                                                                                                                                                                          283416 seqs, 96216763 residues
                                                                                                                                                                                                                                                                                                                                                                                                                        March 28, 2006, 13:15:18;
                                                                                                                                                                                                                                                                                                                          MAPRGFSCLLLLTSEIDLPVKRRA 24
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Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                               summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

A; Molecule type: DNA A; Residues: 1-269 < KUR> A; Status: preliminary

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#### SUMMARIES

;	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	ហ	4.	ω	N	_	Result No.
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# ALIGNMENTS

nitroreductase family protein fused to ferredoxin domain [imported] - Clostridium acetobu C; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004 C; Accession: F97327 R; Nolling, J; Breton, G; Omelchenko, M.V; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, P; Nolling, J; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J, Bacteriol. 183, 4823-4838, 2001
A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clost A; Reference number: A96900; MUID:21359325; PMID:21359325

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C;Accession: AF3470

R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesst Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensi A;Reference number: AD3252; PMID:11756688

A;Accession: AF3470
                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-359 <KUR>
A;Cross-references: UNIPROT:Q8YEX9; UNIPARC:UPI00000581B8; GB:AE008917; PIDN:AAL52929.1;
A;Experimental source: strain 16M
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                 transcription regulator [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
                                                                  A;Gene: BMEI1748
A;Map position: I
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    38.3%;
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Pred. No. 3;
    Score 46;
Pred. No.
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A;Access.co...
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q9YFG0; UNIPARC:UPI000005DAA1; DDBJ:AP000059; NID:g5103911;
A;Cross-references: UNIPROT:Q9YFG0; UNIPARC:UPI000005DAA1; DDBJ:AP000059; NID:g5103911;
probable pheromone-responsive regulatory protein S - Enterococcus faecalis plasmid C;Species: Enterococcus faecalis C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Jun-1993 C;Accession: E41662 C;Accession: E41662 R;Kao, S.M.; Olmsted, S.B.; Viksnins, A.S.; Gallo, J.C.; Dunny, G.M. J. Bacteriol. 173, 7650-7664, 1991
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C;Superf
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C56272
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A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy. A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: H72717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prgS protein -
C;Species: Ente
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Genetic analysis of a region of the Enterococcus faecalis plasmid pCF10 involve A;Reference number: A56272; MUID:95238283; PMID:7721703 A;Accession: C56272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Chung, J.W.; Bensing, B.A.; Dunny, G.M. J. Bacteriol. 177, 2107-2117, 1995
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                                                                                                                 E41662
                                                                                                                                   RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-90 < CHU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
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Matches
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;Species: Enterococcus faecalis
;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                      ;Genome: plasmid
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Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
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9; Conserv
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                                                                                                                                                                                                                          CLLLLTSEIDLPVKRRA
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52.9%;
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Pred. No.
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Pred. No. 11;
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hypothetical protein TC0026 [imported] - Chlamydia muridarum (strain Nigg)
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: F81747
R,Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzber Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: F81747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
F81747
                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-107 <TET>
A;Cross-references: UNIPROT:Q9PLR9; UNIPARC:UPI0000057781; GB:AE002271; GB:AE002160; NID
A;Experimental source: strain Nigg (MoPn)
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R;TSo, J.Y.; Zalkin, H.; van Cleemput, M.; Yanofsky, C.; Smith, J.M.
J. Biol. Chem. 257, 3525-3531, 1982
A;Title: Nucleotide sequence of Escherichia coli purF and deduced amino A;Reference number: A92366; MUID:82142516; PMID:6277938
A;Accession: A04446
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C;Species: Escherichia coli
C;Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 31-Dec-2004
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                                                                                                                                                                                                                                                               A;Status: preliminary
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A; Residues: 1-92 <TSO>
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A; Residues: 1-90 < KAO>
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PRGFSCLLLLTSEIDLPVK 21
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                                                                                                                               Chlamydia muridarum hypothetical protein TC0026
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Salzberg,
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*hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: 876234
C;Accession: 876234
RESULT 10

Ba2891

beta-galactosidase (EC 3.2.1.23), 36K chain - Leuconostoc lactis (strain NZ6009)

C;Species: Leuconostoc lactis

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C;Accession: B42891

R;David, S.; Stevens, H.; van Riel, M.; Simons, G.; de Vos, W.M.

J. Bacteriol. 174, 4475-4481, 1992

A;Title: Leuconostoc lactis beta-galactosidase is encoded by two overlapping gene A;Reference number: A42891; MUID:92325034; PMID:1624440

A;Accession: B42891
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A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A:Reference number: AB1807; MUID:21595285; PMID:11759840
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A;Cross-references: UNIPROT:P74396; UNIPARC:UPI00000C0E76; EMBL:D90914;
A;Note: the nucleotide sequence was submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
A; Molecule type: DNA
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A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
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A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-1796 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: AB1807;
A;Accession: AC1895
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Pred. No. 1.3e+02;
1; Mismatches 7
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A;Note: this accession replaces C;Genetics: A;Gene: PH1206
                                                                                                                                                                                                                                 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Y
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: H71063
                                                                                                                                                                                                                                                                                                                                                         hypothetical protein PH1206 - Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004 C;Accession: H71063
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A;Introns: 4/3; 53/3; 209/3; 962/1; 1632/1; 1686/2; 1739/1; 1793/1
A;Note: EG:52C10.5
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C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision
C;Accession: T13576
R;Benos, P.
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A;Cross-references: UNIPROT:Q02604; UNIPARC:UPI00001268F5; GB:M92281; NID:g149634; PIDN:C;Keywords: glycosidase; hydrolase
                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown; translation A;Molecule type: DNA A;Residues: 1-170 <KAW>
                                                                                                                                     A;Cross-references: UNIPROT:058978; UNIPARC:UPI0000063002; A;Experimental source: strain OT3
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A; Residues: 1-1854 <BEN>
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                                                                                                                                                                                                                                                                                                             Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino,
4.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki,
                                       Query Match
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Score 43; DB Pred. No. 18; 2; Mismatches
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J.; Kushida,
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C;Date: 13-bey....
C;Accession: B71566
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marau...,
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marau...,
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marau...,
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marau...,
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; F
                              C;Accession: H97244

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.; Bacteriol. 183, 4823-4838, 2001

J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: H97244
                                                                                                                                                                                                                                                      membrane associated methyl-accepting chemotaxis protein [imported] - Clostridium C;Species: Clostridium acetobutylicum c;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 C;Accession: H97244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: G83589

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, i, Lory, S.; Olson, M.V.
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A;Reference number: A82950;
A;Accession: G83589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-359 < ARN>
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A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                H97244
                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: PA0450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-540 <S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable phosphate transporter PA0450 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: UNIPROT:Q91668; UNIPARC:UP100000C5060; GB:AE004482; GB:AE004091; Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary
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Accession: G83589
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ilarity 50.0%;
Conservative
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50; MUID:20437337; PMID:10984043
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Pred. No. 57;
2; Mismatches
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                                                                                                               Solvent-Producing Bacterium
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A.; Larbig,
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K.; Lim,
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A;Molecule type: DNA
A;Residues: 1-570 <KUR>
A;Residues: 1-570 <KUR>
A;Residues: 1-570 <KUR>
A;Cross-references: UNIPROT:Q97FD7; UNIPARC:UPI00000CA63B; GB:AE001437; PIDN:AAK80747.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2803
밁
                        á
                                                                     Query Match
Best Local (
                                                         Matches
350 KGFDCILQLQNAVDKNIK 367
                            4 RGFSCLLLLTSEIDLPVK
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                                                         Conservative
                                                                     35.8%;
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                            21
                                                                     Score 43;
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Search completed: March 28, 2006, 13:20:56 Job time: 4.136 secs

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Gapop 10.0 , Gapext 0.5
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120
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     GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration
                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUNIN HUMAN
Q97DJ4 CLOAB
Q55X85 CRYNE
Q5KMP8 CRYNE
Q5KMP8 AZOCA
Q8FMY9 COREF
                    Q64BIG PARCH
Q59V29 CANAL
Q8ZT01 PYRAE
Q9ZT01 AERPE
Q9YFG0 AERPE
Q57ZB4 9TRYP
Q54Q18 DICD1
Q943G2 ORYSA
Q59UP4 CANAL
Q70PV8 GIALA
                                                                                                                                                                                 Q5F9G4 PONPY
Q89E87 BRAJA
Q89E87 BMENI
Q89E87 BMENI
Q4NML4 9MICC
Q6LP76 PLAF7
Q59UZ3 CANAL
Q59E17 BRUMB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s Swiss-Prot entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EV European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the access of FPRLI to APP. Prevents the translocation of BAX cytosol to mitochondria.
SUBUNIT: Interacts with IGFBP3, BAX and TRIM11.
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Expressed in the heart, skeletal muscles,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the hippocampus.
INDUCTION: Release is regulated by i
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Noelling J., Breton G., OmeLchenko M.V., Makarova K.S., Zeng Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P., Daly M.J., Bennett G.N., Koonin B.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-proclamaterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
EMBL, AB007945; AAK81409.1; -; Genomic_DNA.
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Pfam; PF000353; 4FE4SPRDOXIN.
                  Cryptococcus neoformans var. neo
Eukaryota; Fungi; Basidiomycota;
Tremellomycetidae; Tremellales;
                                                                                 Hypothetical protein. ORFNames=CNBB4770;
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STRAIN=ATCC 824 / DSM 792 / VKM B-MEDLINE=21359325; PubMed=11466286;
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Pred. No. 4.9e-12;
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                    Tremellaceae;
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                                                                                                                                         Loftus B.J., Fung B., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
RA Bosdet I.E., Brent M.R., Chiu R., Doerling T.L., Donlin M.J.,
RA D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,
RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,
RA Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E.,
RA Mathewson C.A., Mitchell T.G., Pertea M., Riggs F.R., Salzberg S.L.,
Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
RA Schein J.E., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,
RA Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,
Fraser C.M., Hyman R.W.,
Fraser C.M., Hyman R.W.,
Science 307:1321-1324(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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10-MAY-2005
10-MAY-2005
10-MAY-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cryptococcus neoformans var. neof
Bukaryota; Fungi; Basidiomycota;
Tremellomycetidae; Tremellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cryptococcus neoformans serotype D sequencing.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
-i- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (MGS) entry v
                                              EMBL; AB017342; AAW41793.1; -; Interpro; IPR011989; ARM-like. Interpro; IPR001357; HEAT. Pfam; PF02985; HEAT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein. ORFNames=CNB00940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
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Wickes B.L., Fu J., Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=15653466; DOI=10.1126/science.1103773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-JEC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-2005) to
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Van Aken S.,
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6; AAEY01000011; EAL22302.1; -; Genomic_DNA.
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                       proteome;
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(MAY-2004)
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     1181 AA;
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     Hypothetical ; 130134 MW;
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Pred. No. 1.1e
5; Mismatches
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                                                                                                                      Genomic_DNA
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825BF00F2CDD4C00 CRC64;
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QBFMY9;
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01-MAR-2003 (TrEMBLre:
01-JUN-2003 (TrEMBLre:
Putative carboxylase.
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05-JUL-2004
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baginsky C., Palacios J.M., Imperial J., Ruiz-Argueso T., "Molecular and functional characterization of the Azorhizo caulinodans GRS571 hydrogenase gene cluster."; FEMS Microbiol. Lett. 237:399-405 (2004).

EMBL; AY581127; AA591029:1; -; Genomic DNA.
GO; GO:0009375; C:ferredoxin hydrogenase complex; IEA.
GO; GO:0004672; F:metal ion binding; IEA.
GO; GO:0004672; F:metalloendopeptidase activity; IEA.
GO; GO:0004222; F:metalloendopeptidase activity; IEA.
GO; GO:0016485; P:protein processing; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGREAMS; TIGR00140; hupD; 1.
TIGREAMS; TIGR00141; hupD_frhD_pept; 1.
TIGREAMS; TIGR00072; hydrog_prot; 1.
TIGREAMS; TIGR00072; hydrog_prot; 1.
SEQUENCE 208 AA; 22061 MW; 75CC7B4B280B3724 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hyphomicrobiaceae; Azorhizobium.
MCBI_TaxID=7;
                            OrderedLocusNames=CE2360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0004222; F:metalloendopeptidase act GO; GO:0016485; P:protein processing; IEA. InterPro; IPR000671; Peptidase M52. InterPro; IPR0004419; Pept_M52_HybD. InterPro; IPR004271; Pept_M52_mat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22335395; PubMed=12324339; DOI=10.1128/ARM.68.10.4915-4924.2002; DOI=formary C., Brito B., Imperial J., Palacios J.N Baginsky C., Brito B., Imperial J., Palacios J.N "Diversity and evolution of hydrogenase systems Appl. Environ. Microbiol. 68:4915-4924(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=hupD;
Azorhizobium caulinodans.
Bacteria; Proteobacteria;
    Corynebacterium efficiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01750; HycI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=15321689; DOI=10.1016/j.femsle.2004.07.003;
Baginsky C., Palacios J.M., Imperial J., Ruiz-Argu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hupb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00446; HYDRGNUPTAKE.
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                                                                                                                (TrEMBLrel.
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                                                                                         (TrEMBLrel.
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Pred. No.
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1.1e+02;
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27;
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collaboration

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DPF3_CHICK
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Matches 11
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Genome Res. 13:1572-1579 (2003).

L Genome Res. 13:1572-1579 (2003).

R EMBL; BA000035; BAC19170.1; -; Genomic DNA.

R GG; GO:0009320; C:phosphoribosylaminoimidazole carboxylase (GG; GO:0009576; F:nucleic acid binding; IEA.

R GG; GO:000452; F:pancreatic ribonuclease activity; IEA.

R GG; GO:000452; F:pancreatic ribonuclease activity; IEA.

R GG; GO:000463; F:phosphoribosylaminoimidazole carboxylase (GG; GO:000468); F:phosphoribosylaminoimidazole carboxylase (R); GO:0006189; P:'de novo' IMP biosynthesis; IEA.

R InterPro; IPR000031; AIR_carboxyl.

R InterPro; IPR0001427; RNaseA.

R ProDom; PD002193; AIR_carboxyl; 1.

Complete proteome.

Complete proteome.
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P58270;
16-OCT-2001 (Rel. 40, C
16-OCT-2001 (Rel. 40, L
10-MAY-2005 (Rel. 47, L
                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2; 3 AND 4)

MEDLINE-21833813; PubMed-11845289; DOI=10.1007/s00335-001-3039-1;

Ninkina N.N., Mertealov I.B., Kuilkova D.A., Alimova-Kost M.V.,

Simonova O.B., Korochkin L.I., Kiselev S.L., Buchman V.L.;

"Cerd4, third member of the d4 gene family: expression and organization of genomic locus.";

Mamm. Genome 12:862-866(2001).

-!- FUNCTION: Probably involved in RNA transcription.

-!- SUBCELULURAR LOCATION: Nuclear and cytoplasmic (Potential).

-!- ALTERNATIVE PRODUCTS:
                       +++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence up 10-MAY-2005 (Rel. 47, Last annotation Zinc-finger protein DPF3 (cer-d4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nishio Y., Nakamura Y., Kawarabayasi Y
Sugimoto S., Matsui K., Yamagishi A.,
Gojobori T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLECTIDE SEQUENCE: NUCLECT DE MEDITALE STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
MEDITALE=22733752; PubMed=12840036; DOI=10.1101/gr.1285603;
Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E.,
Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=DPF3; Synonyms=CERD4;
Gallus gallus (Chicken).
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Corynebacterinaae; Corynebacteriaceae; Corynebacterium.
                       SIMILARITY:
SIMILARITY:
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                    Event=Alternative
                                                                                                                 IsoId=P58270-4;
                                                                                                                                                                       IsoId=P58270-3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                       270-4; Sequence=VSP_005614, VSP_005
Belongs to the requiem/DPF famIly.
Contains 1 C2H2-type zinc fingers.
Contains 2 PHD-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.0%;
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ole for the thermostability of Corynebacterium
                                                                                                                                                                    Sequence=VSP_005614,
                                                                                                                                                                                                                            Sequence=VSP_005614,
                                                                                                                                                                                                                                                                                                                                              splicing; Named isoforms=4;
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Pred. No.
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                                                                                                              005615,
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ENSEMBL; ENSCALGO000009352; Gallus gallus.

InterPro; IPR000637; AT hook DNA bd.

InterPro; IPR007087; Znf C2H2.

InterPro; IPR001965; Znf PHD.

InterPro; IPR001965; Znf PHD.

InterPro; IPR001965; Znf RING.

Pfam; PP00628; PHD; 2.

Pfam; PP00628; PHD; 2.

PFRINTS; PR00929; ATHOOK.

SMART; SM00249; PHD; 2.

SMART; SM00194; RING; 2.

SMART; SM00194; RING; 2.

SMART; SM00195; ZPF PHD 1; 1.

PROSITE; PS00159; ZF PHD 2; 2.

SMART; SM00259; ZNF CSH2; 1.

PROSITE; PS00159; ZF PHD 2; 2.

PROSITE; PS00159; ZF PHD 2; 2.

PROSITE; PS00159; ZF PHD 2; 2.

PROSITE; PS00159; ZF PHD 3; 2.

PROSITE; PS00159; ZF PHD 3; 2.

PROSITE; PS00159; ZF PHD 3; 1.

PROSITE; PS00159; ZF PHD 3; 2.

PROSITE; PS00159; ZF PHD 3; 1.

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PROSITE; PS00159; ZF PHD 3; 1.

PROSITE; PS00159; ZF PHD 3; 2.

PROSITE; PS00159; ZF PHD 3; 1.

PROSITE; PS00159; ZF PHD 3; 2.

PROSITE; PS00159; ZF PHD 3; 2.

PROSITE; PHD 3; 2.

PROS
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last amoutation updat
Hypothetical protein DKFZp469B1012.
Name=DKFZp469B1012;
The German cDNA Consortium; Wambutt R., Heubner D., Mew Fobo G., Han M., Wiemann S.
                                                                                                                                                                                                                             Pongo pygmaeus (Orangutan)
Eukaryota; Metazoa; Chorda
Mammalia; Eutheria; Euarch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This Swiss-Prot entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Event the European Bioinformatics Institute. There are no restruse as long as its content is in no way modified and this s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q5R9C4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q5R9C4_PONPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             removed
                                                                                        TISSUE=Kidney;
                                                                                                                                                                  NCBI_TaxID=9600;
                                                                                                                                                                                                      Pongo
                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PONPY 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF362754; AAK51968.1;
AF362753; AAK51967.1;
AF362756; AAK51970.1;
AF362755; AAK51969.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       long as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGFSCLLLLTSBIDLPVKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRFLSCKLYTSEVDLPLKK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247
308
365
102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₽,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              427
                                                                                                                                                                                                                          Chordata; Craniat.
Euarchontoglires;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48930 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.0%;
52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 68
                                   Mewes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB Pred. No. 56; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulation; Zinc; C2H2-type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Missing (In isoform 2 and isoform 4).
/FTId=VSP_005615.
GHPTCLQFTTNMTEAVKTYQWQCIECKSCSLCGTSENDDQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Missing (in isoform 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isoform 3 and isofo
/FTId=VSP 005616.
B22DB85D1E714152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LFCDDCDRGYHMYCLNPPVFEPPEGSWSCHLCRELLRERAS
AFGFQA -> AHLGREGRRDEAAPTRTTEDLFGSTSESDTS
TFHGFDEDDAEEPLSSRGGGCGGSSESADKKGGC (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHD-type 1.
PHD-type 2.
                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
oglires; Primates; Catarrhini; Homin
                                   ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'FTId=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA.
mRNA.
mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                   Weil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            542
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_005616.
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                                   B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ξ
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                                   Amid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 427,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zinc-finger.
                                                                                                                                                                                                                                      Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ν
                                   ?
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this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
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18
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not
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RESULT 9
Q89E87] BRAJA P
Q89E87]
AC
Q89E87;
D7
O1-UNN-2003 (T
D7
O1-UNN-2003 (T
D7
O1-WAR-2004 (T
D8
B117200 proted
GN
OrderedLocuseNa
OS
Bradyrhizobiam
OC
STRAIN-32484
RA
Kaneko T., Nak
RA
Kaneko T., Nak
RA
Kaneko T., Nak
RA
Fabata S., W
RA
Kohara M., Mat
RA
Tabata S., W
RA
TABATA Sasamoto S., W
RA
TABATA SASAMOTO
RO
GO:0006811
DR
DR
GO; GO:0006811
DR
DR
InterPro; IPR(
DR
DR
Pfam; PF00496;
DR
PFOSITE; PS000(
KW
Complete prote(
SQ
SEQUENCE
S2
SEQUENCE
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                                                                   Query Match
Best Local S
Matches 11
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Best L
                                                                                                                                     Bradyrhizobium japonicum USDA110.";

DNA Res. 9:189-197(2002).

EMBL; BA000040; BAC52465.1; -; Genomic_DNA.

GO; GO:0005215; F:transporter activity; IEA.

GO; GO:0006810; P:transport; IEA.

InterPro; IPR006914; SBP_bac_5.

InterPro; IPR006311; Tat.

Complete proteome.

SEQUENCE 527 AA; 57740 MW; 7ECBE31BFB1COFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:000524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0015075; F:ion transporter activity; IEA.
GO; GO:0015293; F:symporter activity; IEA.
GO; GO:0006811; P:ion transport; IEA.
GO; GO:0006814; P:sodium ion transport; IEA.
GO; GO:0006814; P:sodium ion transport; IEA.
InterPro; IPR001714; MFS.
InterPro; IPR001714; MFS.
InterPro; IPR005179; Sug transporter.
Pfam; PF07690; MFS 1; 1.
PROSITE; PS00809; 2A0119; 1.
PROSITE; PS00816; SUGAR_TRANSPORT_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
EMBL; CR85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=USDA 110;
MEDLINE=22484998; PubMed=12597275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OrderedLocusNames=bl17200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bl17200 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 542 AA; 59847 MW; FAF2E14949E711B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashi
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                               Complete genomic sequence of nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                   l Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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PRGYACMLRLNHLQPPFDNPAVRRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRGFSCLLLLTSEI 16
                                 PRGFSCLLLLT---SEIDLPVKRRA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NOV-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                39.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24,
                                                                 Score 47.5; D
Pred. No. 84;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence up
Last annotation
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Pred. No. 71;
                                                                                                                                                                                                                                                                                                         activity; IEA.
                                                                                                                                           7ECBE31BFB1C0FC5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                527
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                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Length 542;
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                                                                     8
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                                                                                                                                           CRC64;
                                                                                                     Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                     Indels
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ada T., Yamada M.,
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                                                                   Gaps
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RESULT 11
Q4NML4 9MICC
ID Q4NML4 9
AC Q4NML4;
DT 13-SEP-2
DT 13-SEP-2
DT 13-SEP-2
DT 13-SEP-2
DT 08-FNames
OS ARTHOODA
OC M1CTOCOC
OX NCB1 Tax
RN NUCLEOTI
RC STRAIN=F
RG US DOE J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook P., Corum B., DeArellano K.,
RA Choepel Y., Collymore A., Cook P., Corum B., DeArellano K.,
RA Choepel Y., Collymore A., Cook P., Corum B., DeArellano K.,
RA Choepel Y., Collymore A., Cook P., Corum B., DeArellano K.,
RA Choepel Y., Collymore A., Cook P., Corum B., DeArellano K.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Hagopian D., Hagos B., Hall J., Horton L., Kamat A., Karatas A.,
RA Kells C., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kals C., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
RA Mathews C., Maucell B., McCarthy M., Meldrim J., Meneus L.,
RA Milova T., Mlenga V., Murphy T., Naylor J., Myuyen C., Nicol R.,
RA Milova T., Mlenga V., Murphy T., Naylor J., Myuyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA Milova T., Mlenga V., Bramson Y., Schupback R., Seaman S., Severy P., Smirnov S.,
RA Rachupka A., Ramsamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Ramas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Manda J., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
Wall C., Wang S., Wilson B.,
Wall C., Wang S., Viel R., Vo A., Wang S., Wilson B.,
Wall C., Wang G., Zainoun J., Zembek L., Zimmer A., Zody M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                  QANML4 9MICC PRELIMINARY; PRT; 532 AA.

Q4NML4;

13-SEP-2005 (TrEMBLrel. 31, Created)

13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

Similar to Sugar diacid utilization regulator.

ORFNames=ArthDRAFT 3900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome Sequence of Aspergillus nidulans.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ
EMBL; AACD01000043; EAA64707.1; -; Genomic_DNA
GO; GO:0016787; F:hydrolase activity; IEA.
                                                                                                                           Arthrobacter sp. FB24.
Bacteria, Actinobacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aspergillus nidulans FGSC A4.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
    STRAIN=FB24;
US DOE Joint Genome Institute (JGI-PGF);
                                              NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein. ORFNames=AN2602.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAY-2005 (TrEMBLrel.
10-MAY-2005 (TrEMBLrel.
10-MAY-2005 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q5BA28 EMENI PRELIMINARY;
Q5BA28;
                                                                                   NCBI_TaxID=290399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000379; Ser_estrs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-FGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                   13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSEIDLPVKRRA 24
                                                                                                                                                                                                                                                                                                                                                                                                         TSEIQIPLKRRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical proteing 387 AA; 42761 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.2%;
ilarity 75.0%;
Conservative
                                                                                                         Micrococcaceae;
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                                                                                                                                 Actinobacteridae; Actinomycetales;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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A Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
A Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
A Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
A Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
A Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
A Cronin A., Bayles R., Boodhead I., Gwilliam R., Hamlin N., Hance Z.,
A Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
A Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
A Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
A Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
A Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
A Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
A Cliver K., Ormond D., Price C., Quall M.A., Rabbinowitsch E.,
A Oliver K., Ormond D., Price C., Quall M.A., Rabbinowitsch E.,
A Seger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
A Seger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
A Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
L., Nature 419:527-531(2002).
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Hammon N., I.
"Sequencing of Submitted (J)
[2]
Cherevach I., Davis P., Goodhead I., Stevens K., Mungall K., Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Dogge. Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.G; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; CRAS2400, CAC25050.1; -; Genomic_DNA.

GO; GO:0004714; F:ATP binding; IEA.

GO; GO:0004714; F:protein serine/threonine kinase activity; IEA.

GO; GO:0004715; F:protein-tyrosine kinase activity; IEA.

GO; GO:0004715; P:protein amino acid phosphorylation; IEA.

InterPro; IPR0002190; Ser_Thr_pkinase.
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Q6LF76;
Q5-JUL-2004 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein (Protein kinase, putative).
ORFNames=PFF1145c;
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"Annotation of the draft genome Submitted (JUN-2005) to the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
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US DOE Joint Genome Institute (PGF-ORNL);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22255708; PubMed=12368867; DOI=10.1038/nature01095;
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; AAHG01000001; E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLGFASLILRPSRADSPIER
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Pred. No. 1e+0
4; Mismatches
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RESULT
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OB6126\_BRAJA PRELIMINARY; PRT; 163 AA. 086126; Q79V08; O1-NOV-1998 (TrEMBLrel. 08, Created) O1-NOV-1998 (TrEMBLrel. 08, Last sequence update) 13-SEP-2005 (TrEMBLel. 31, Last annotation update) Hypothetical protein (B170903 protein). OrderedLocusNames=blr0903;

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SMART; SM00220; S.TKC; 1.

SMART; SM00219; TyrKC; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

Hypothetical protein; Kinase.

SEQUENCE 2404 AA; 279784 MW; EE0162E
                                                                                EMBL; AACQ01000127; E
Hypothetical protein.
SEQUENCE 106 AA; 1
                                                                                                                        "Annotation of the Genome of Candida albicana.";
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-i- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry v
                                                                                                                                                                                                                        Candida albicans SC5314.
Eukaryota; Fungi; Ascomycota;
Saccharomycetales; mitosporic
NCBI_TaxID=237561;
                                                                                                                                                                 Dungan J., Kuo A., Newport G., Lan C. Roberts J., Persson K., Donnelly S., Jones T., Scherer S., Agabian N.;
                                                                                                                                                                                                                                                              PubMed=15123810; DOI=10.1073/pnas.0401648101;
Jones T., Federspiel N.A., Chibana H., Dungan J.,
Magee B.B., Newport G., Thorstenson Y.R., Agabian
                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
STRAIN=SC5314;
                                                                                                                                                                                                                                                                                                                                                                 hypochetical protein. ORFNames=CaO19.3748;
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10-MAY-2005
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                                                                                                                                                                                                                                                                                                                                                                            Hypothetical
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                                                                                                    preliminary data.; AACQ01000127; E
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                                       l Similarity
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Pred. No.
                                                  Score 46;
Pred. No.
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                                                                                                    Genomic_DNA.
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Favoreto S., Tzung
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                                                            Length 106;
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N., Mag
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RESULT 15
Q57FH7 BRUAB
ID Q57FH7 B
AC Q57FH7 B
AC Q57FH7 B
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O-MAY-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=9-941 / Biovar 1;
PubMed=15805518; DOI=10.1128/JB.187.8.2715-2726.2005;
Halling S.M., Peterson-Burch B.D., Bricker B.J., Zuerner R.L.,
Qing Z., Li L.-L., Kapur V., Alt D.P., Olsen S.C.;
"Completion of the genome sequence of Brucella abortus and comparison to the highly similar genomes of Brucella melitensis and Brucella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; AJ006100; CAA06860.1; -; Genomic DNA.
EMBL; BA000040; BAC46168.1; -; Genomic DNA.
InterPro; IRR099394; DUF1052.
Pfam; PF06319; DUF1052.
Pfam; PF06319; DUF1052.1.
Complete proteome; Hypothetical protein.
SEQUENCE 163 AA; 18262 MW; 19213ZE003DE83D6 CRC64;
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MEDLINE=98349447; PubMed=9683482;
Bauer B., Kaspar T., Fischer H.M., Hennecke H.;
"Expression of fixEnifA operon in Bradyrhizobium japonicum depends
a new response regulator system, RegR.";
J. Bacteriol. 180:3853-3863(1998).
                                                                                                                                                                                                                                                                                                                       Complete proteome.
SEQUENCE 322 AA; 34746 MW; 2C912CFFE235402A CRC64;
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EMBL; AB017223; AAX73607.1; -; Genomic_DNA.
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
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STRAIN=USDA 110;
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
NCBI_TaxID-375;
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%; Pred. No. 90;
3; Mismatches
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Search completed: March 28, 2006, 13:20:02 Job time: 21.008 secs THIS PACE OF MAN USERIA

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Result
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1: /cgm2_6/ptodata/1
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US-09-489-039A-11748
US-09-489-039A-11748
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	4, Appli	207, App	<ol><li>Appli</li></ol>	4, Appli	20739, 1	-	72, Appl	31986, 4	19237, A	-	78, Appl	-	•	81, Appl	82, Appl	83, Appl	84, Appl

### ALIGNMENTS

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Sequence 16093, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
APPLICANT: Kealth Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO C
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT PILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 16093

LENGTH: 460

TYPE: PRT
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PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 11091
LENGTH: 466
TYPE: PRT
ORGANISM: Myxococcus xanthus
US-09-902-540-11091
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US-09-248-796A-16093
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Sequence 18594, Application.

Patent No. 6551795

Patent Information:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: MICLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                  PRIOR APPLICATION NOWBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NOWBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17622
LENGTH: 178
                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: MATC J. RUBENFIELD et al.
APPLICANT: MATC J. RUBENFIELD et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
FILE REFERENCE: 107196.136
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Best Local Similarity 4/...
Conservative
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SEQ ID NO 18594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa
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                                                                                          Local Similarity
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Local Similarity 47.4%;
tes 9; Conservative
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88 LVLRERLDLPVRRR 101
                                   10 LLITSEIDLPVKRR 23
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                                                                        Conservative
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IBER: US 60/074,788
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57.1%;
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; Pred. No. 22;
3; Mismatches
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                                                                                          Score 43; DB Pred. No. 16;
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Pred. No. 13;
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                                                                                                           SEQ ID NO 22560
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Best Local Similarity
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GENERAL INFORMATION:
                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                            PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-
                                                                                                                                                                                                                                                            APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-720-2441 INFORMATION FOR SEQ ID NO: 2:
                                                         ORGANISM: Pseudomonas aeruginosa
                                                                                         LENGTH: 597
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TYPE: amino acid
TOPOLOGY: line
WOLECUE
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LENGTH: 537 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: BOTTELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/647,397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Beier,
APPLICANT: Brady,
TITLE OF INVENTION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Kevin P.
GSTEOCLAST TRANSPORTER
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Pred. No.
   Score 43;
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60;
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Length 597;
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RESULT 8
US-09-489-039A-11748
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Sequence 11748, Application US/09489039A

Batent No. 6610836

GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A
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Best Local (
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INFORMATION FOR SEQ ID NO: 4:
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NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: B080
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Beier,
APPLICANT: Brady,
                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 11near MOLECULE TYPE: prot
                                                                                                                                                                                                                                                                                                                                                                     MOLECULE YES
ANTI-SENSE: NO
ANTI-SENSE: NO
internal
                                                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE: internal ORIGINAL SOURCE: ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 617-720-2441
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les 8; Conserv
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Brady, Kevin P.
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72.7%;
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CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60.
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11748
LENGTH: 138
TYPE: PRT
                                                                ; ORGANISM: Myxococcus xanthus US-09-902-540-15112
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US-09-614-891-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-614-891-10
                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
                                                                                                NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 15112
LENGTH: 338
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                             Sequence 15112, Application US/09902540 Patent No. 6833447
Query Match
Best Local Similarity
Matches 8; Conserv
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APPLICANT: SUN, WILLIAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: ORGANIC ANION TRANSPORTER GENES AND PROTEINS FILE REFERENCE: 030727.0022.CIP.1 CURRENT APPLICATION NUMBER: US/09/614,891 CURRENT FILING DATE: 2000-07-12 PRIOR APPLICATION NUMBER: 60143,771 PRIOR FILING DATE: 1999-07-12 NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 542
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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 Score 41.5; D
Pred. No. 63;
6; Mismatches
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; Sequence 19, Application US/091; Pattent No. 6387657; GENERAL INFORMATION: APPLICANT: Botstein, David A.; APPLICANT: Cohen, Robert; APPLICANT: Goddard, Audrey; APPLICANT: Gurney, Austin L.
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Best Local Similarity
"hes 9; Conserv?
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                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 9041
LENGTH: 155
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9041
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12316
LENGTH: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: INFERTON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: ENEUMONIAB FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9041, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2000-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/117,747 PRIOR FILING DATE: 1999-01-29
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Local Similarity 36.8%;
nes 7; Conservative
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                                                                                                               Application US/09182145B
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                                                         David A.
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75.0%;
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Pred. No. 30;
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Pred. No. 21;
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CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1997-10-29
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: US 60/081,695
EARLIER FILING DATE: 1998-04-14
EARLIER FILING DATE: 1998-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Lawrence, David A.
APPLICANT: Levine, Arnold J.
APPLICANT: Pennica, Diane
APPLICANT: Roy, Margaret Ann
APPLICANT: Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Botstein, David
APPLICANT: Cohen, Robert
APPLICANT: Goddard, Audrey
                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
SEQ ID NO 99
LENGTH: 229
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SEQ ID NO 19
LENGTH: 228
                                                                            Matches
                                                                                                              Query Match
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Best Local (
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                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/182,145B
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: US 60/063,704
EARLIER FILING DATE: 1997-10-29
EARLIER APPLICATION NUMBER: US 60/073,612
EARLIER FILING DATE: 1998-02-04
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: US 60/081,695
EARLIER FILING DATE: 1998-04-14
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APPLICANT: Pennica, Diane
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
ITITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: P1176R2
CURRENT APPLICATION NUMBER: US/09/182.145R
                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME FILE REFERENCE: P1176R2
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TYPE: PRT
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                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                            Local
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105 GFTCLPLCSEDVRLP 119
                                    5 GFSCLLLLTSEIDLP 19
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Similarity 46.7%;
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                                                                            Conservative
                                                                                            34.2%;
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Pred. No.
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US-09-182-145-98

Sequence 98, Application US/09182145B

Sequence 98, Application US/09182145B

RESULTANT No. 6387557

GENERAL INFORMATION:

APPLICANT: General Abert

APPLICANT: Horsence, David A.

APPLICANT: Horsence Javid A.
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Minimum
Maximum
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Maximum Match 100%
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1: pir1:*
2: pir2:*
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## ALIGNMENTS

A;Cross-references: UNIDARC:UPI00000012D0; GB:M88107; NID:g189862; PID:g189863
A;Experimental source: granulocytes
A;Note: formyl peptide-stimulated calcium mobilization comparable to that of the formyl R;Murphy, P.M.; Ozcelik, T.; Kenney, R.T.; Tiffany, H.L.; McDermott, D.; Francke, U. J.; Tiblo. Chem. 267, 7637-7643, 1992
A;Tible: A structural homologue of the N-formyl peptide receptor. Characterization and A;Reference number: A42492; MUID:92218423; PMID:1373134
A;Reference number: A42492; MUID:92218423; PMID:1373134 A;Cross-references: UNIPARC:UPI0000012D0; GB:M84562; NID:g182741; PIDN:AAA52473.1; A;Note: sequence extracted from NCBI backbone (NCBIN:94159, NCBIP:94160)
R;Nomura, H.; Nielsen, B.W.; Matsushima, K.
Int. Immunol. 5, 1239-1249, 193
A;Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte A;Reference number: I54751; MUID:94092629; PMID:7505609
A;Accession: I54751 A;Cross-references: UNIPARC:UPI0000012D0; EMBL:X63819; NID:g31460; PID:g31461
A;Experimental source: bone marrow mENA
R;YE, R.D.; Cavanagh, S.L.; Quehenberger, O.; Prossnitz, E.R.; Cochrane, C.G.
Biochem. Biophys. Res. Commun. 184, 582-589, 1992
A;Title: Isolation of a cDNA that encodes a novel granulocyte N-formyl peptide receptor.
A;Reference number: JQ1521; MUID:92246937; PMID:1374236
A;Accession: JQ1521 A;Status: nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-351 <PER> Gene 118, 303-304, 1992
A,Title: Cloning of a CDNA encoding a receptor related to the formyl peptide receptor A,Reference number: JC1258, MUID:92380523, PMID:1511907
A,Recession: JC1258 A;Molecule type: DNA
A;Residues: 1-263,'A',265-338,'C',340-351 <BAO>
A;Residues: 1-263,'A',265-338,'C',340-351 <BAO>
A;Rosidues: 1-263,'A',265-338,'C',340-351 <BAO>
A;Cross-references: UNIPROT:P25090; UNIPARC:UPI00001778D8; GB:M76672
A;Note: authors translated the codons GTG for residue 15 as Glu, TCT
R;Perez, H.D.; Holmes, R.; Kelly, B.; McClary, J.; Andrews, W.H.
Gene 118, 303-304, 1992 Genomics 13, 437-440, 1992 A;Title: Mapping of genes for the human C5a receptor (C5AR), human A;Reference number: A42009; MUID:92307681; PMID:1612600 A;Accession: B42009 C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence revision 14-Jul-1995 #text\_change 09-Jul-2004
C;Accession: B42009; JC1258; JQ1521; A42492; I54751; S21581
R;Bao, L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, C. A; Molecule type: mRNA A; Residues: 1-351 < MUR> A; Molecule type: mRNA A; Residues: 1-351 < YE2> A;Status: nucleic N;Alternate names: FMLP receptor homolog FPR2; formyl peptide receptor like-1; probable ( FMLP-related receptor 1 - human **B42009** preliminary; translated from GB/EMBL/DDBJ acid sequence not shown FMLP receptor (FPR), & that of the formyl p.; Francke, U. for residue 19

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A; Molecule type: mRNA
A; Residues: 1-351 cRES'-
A; Cross-references: UNIPARC: UPI0000012D0; GB:D10922; NID:g219864; PIDN:BAA01720.1; PID:
C; Comment: This G-protein coupled receptor, homologous to the N-formyl peptide receptor differentiated myeloid cells and is probably a chemotactic receptor for some other ligan c; Genetics:
A; Genetics: GB:127554; OMIM:136538
A; Genetics: #status absent
C; Superfamily: vertebrate rhodopsin
C; Keywords: Chemotaxis; G protein-coupled receptor; glycoprotein; transmembrane #status predicted <TM1>
F; 59-83/Domain: transmembrane #status predicted <TM2>
F; 100-121/Domain: transmembrane #status predicted <TM5>
F; 206-226/Domain: transmembrane #status predicted <TM5>
F; 206-226/Domain: transmembrane #status predicted <TM5>
F; 206-226/Domain: transmembrane #status predicted <TM7>
F; 282-307/Domain: transmembrane #status predicted <TM5>
F; 282-307/Domain: transmembrane #status predicted <TM7>
F; 4Binding site: carbohydrate (Asn) (covalent) #status predicted <TM7>
F; 98-176/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                FMLP-related receptor 2 - human

N.Alternate names: FMLP-related receptor I; probable chemotactic receptor FPRH2

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C;Accession: C42009

R,Bao, L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, C.

Genomics 13, 437-440, 1992

A;Title: Mapping of genes for the human C5a receptor (C5AR), human FMLP receptor

A;Reference number: A42009; MUID:92307681; PMID:1612600

A;Accession: C42009
A;Cross-references: GDB:128855; OMIM:136539
A;Map position: 19q13.3-19q13.4
A;Introns: #status absent
                                                                                     A; Gene: GDB: FPRL2
                                                                                                                                           A;Molecule type: DNA
A;Rosidues: 1-353 <BAO>
A;Residues: 1-353 <BAO>
A;Cross-references: UNIPROT:P25089; UNIPARC:UPI0000050485; GB:M76673; NID:g182668;
C;Comment: This fMet-Leu-Phe receptor homolog, whose ligand is not yet known, appea
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A;Cross-references: UNIPROT:P21462; UNIPARC:UPI000016A92F; GB:L10820; A;Note: 192-Asn was also found R;Boulay, F.; Tardif, M.; Brouchon, L.; Vignais, P. Biochemistry 29, 11123-1113, 1990 A;Title: The human N-formylpeptide receptor. Characterization of two c A;Reference number: A36309; MUID:91105045; PMID:2176894 A;Accession: A36309
A;Status: not compared with conceptual translation
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                Genomics 13, 437-440, 1992
A;Title: Mapping of genes for the human C5a receptor (C5AR), A;Reference number: A42009; MUID:92307681; PMID:1612600
A;Accession: A42009
                                                                                                       A;Accession: A35495
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-100,'L',102-191,'N',193-350 <BOUZ>
A;Cross-references: UNIPARC:UPI000012AA9F; GB:M37128; NID:g189183
A;Note: the sequence in GenBank entry HUNNFPR, release 112.0, (PII
A;Bao, L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, C.
                                                                                                                                                                                                                                              R;Boulay, F.; Tardif, M.; Brouchon, L.; Vignais, P. Biochem. Biophys. Res. Commun. 168, 1103-1109, 1990 A;Title: Synthesis and use of a novel N-formyl peptide A;Reference number: A35495; MUID:90267449; PMID:2161213
                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPARC:UPI000050484; GB:M60627; GB:M33538; NID:g182664;
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A; Residues: 1-191,'N',193-345,'E',347-350 <BOU1>
A;Status: nucleic acid sequence not shown;
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Pred. No. 4e-1:
39; Mismatches
  not compared with
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A;Cross-references: UNIPARC:UPI000011EA63; GB:S49810; NID:g260832; PIDN:AAD14906.1; PID: C;Genetics:

A;Gene: GB:FPR1
A;Gene: GB:FPR1
A;Gene: GB:FPR1
A;Gene: GB:FPR1
A;Map position: 19q13.4-19q13.4
A;Introns: #status absent
A;Map position: 19q13.4-19q13.4
C;Superfamily: vertebrate rhodopsin
C;Keywords: Chemotaxis; G protein-coupled receptor; glycoprotein; transmembrane protein
C;Keywords: Chemotaxis; G protein-coupled receptor; glycoprotein; transmembrane #status predicted <TM1>
F;27-53/Domain: transmembrane #status predicted <TM2>
F;100-121/Domain: transmembrane #status predicted <TM4>
F;20-525/Domain: transmembrane #status predicted <TM5>
F;206-225/Domain: transmembrane #status predicted <TM5>
F;207-304/Domain: transmembrane #status predicted <TM5>
F;279-304/Domain: transmembrane #status predicted <TM5>
F;279-304/Domain: transmembrane #status predicted <TM7>
F;289-176/Disulfide bonds: #status predicted <TM7>
F;289-176/Disulfide bonds: #status predicted <TM5>
                                                                                                                         N-formyl peptide receptor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46520
R,Ye, R.D.; Quehenberger, O.; Thomas, K.M.; Navarro, J.; Cavanagh, S.L.; Prossnitz,
J. Immunol. 150, 1383-1394, 1993
A;Title: The rabbit neutrophil N-formyl peptide receptor. cDNA cloning, expression,
A;Reference number: A46520; MUID:93163563; PMID:8432984
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A;Title: Cloning of the gene coding for a human receptor A;Reference number: I52414; MUID:93075765; PMID:1445895 A;Accession: I52414
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Residues: 1-352 <YEL's A;Cross-references: UNIPROT:Q05394; UNIPARC:UPI000012AAA3; GB:M
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A; Residues: 1-5 < PER>
                                                                                                         A;Accession: A46520
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  UNIPROT: Q05394; UNIPARC: UPI000012AAA3; GB: M94549; NID: g165027;
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     PIDN:
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N-formyl peptide chemotactic receptor - mouse
(;Species: Mus musculus (house mouse)
(;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
(;Accession: A49542
R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 269, 25395-25401, 1993
J. Biol. Chem. 269, 25395-25401, 1993
A;Title: Species and subtype variants of the N-formyl peptide chemotactic realization of the N-formyl peptide chemotactic realizations.
A;Accession: A49542; MUID:94064602; PMID:8244972
A;Accession: A49542
                                                                                                                                                                                                                                                                                                                                                                           A;Introns: #status absent C;Superfamily: vertebrate C;Keywords: chemotaxis; t
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A;Note: sequence extracted from NCBI backbone (NCBIP:124908)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor: transmembrane profes
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C;Genetics:
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A; Residues: 1-364 < GAO>
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 237; Conserv
                                                                                                                                                                                                                                                                                                                                                                           Superfamily: vertebrate rhodopsin; Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Keywords: G protein-coupled receptor; transmembrane protein
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FRMTRTVTTICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGS
                                                                                                                                                                                                                     MDTNMSLLMNKSAVNLMNVSGSTQSVSAGYIVLDVFSYLIFAVTFVLGVLGNGLVIWVAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLRVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLN
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                                                                         VFLIALIALDRCICVLHPVWAQNHRTVSLAKKVIIVPWICAFLLTLPVIIRLTTV--PNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLRVLSFVVASFLLCWSPYQIAALIATVRIRELLL-GMGKDLRIVLDVTSFVAFFNSCLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.3%;
67.7%;
                                                                                                                                                                                                                                                                                                                    64.6%; Score 1174.5; DB 2; 64.6%; Pred. No. 4.6e-91;
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                                                                                                                                                                                                                                                                                                     Mismatches
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RESULT 6
JC5498
JC5498
G protein-coupled receptor DEZ - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-ul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-200
C;Accession: JC5498
R;Methner; A.; Hermey, G.; Schinke, B.; Hermans-Borgmeyer, I.
Biochem. Biophys. Res. Commun. 233, 336-342, 1997
A;Title: A novel G protein-coupled receptor with homology to neuropeptide.
A;Reference number: JC5498; MUID:97289630; PMID:9144535
A;Contents: Brain
A;Accession: JC5498; MUID:97289630; PMID:9144535
A;Gross-references: UNIPROT:P97468; UNIPARC:UDI00000269A9; GB:U79525; NID:C;Comment: This protein is involved in the bone metabolism.
C;Superfamily: vertebrate rhodopsin
F;110-187/Disulfide bonds: #status predicted
anaphylatoxin C3a receptor - rat C3a pecies: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004 C;Accession: JC5835 R;Fukuoka, Y.; Ember, J.A.; Hugli, T.E. Blochem. Biophys. Res. Commun. 242, 663-668, 1998 Blochem. Biophys. Res. Commun. 242, 663-668, 1998 A;Title: Cloning and characterization of rat C3a receptor: Differential expression A;Reference number: JC5835; MUID:98125550; PMID:9464274
A;Accession: JC5835
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JC5835
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                                                                                                                                                                                                                                                                                            ANSCMNPILYVFMGHDFRKFKV-ALFSRLANALSEDTGPSS 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L--AAPESSPHPÄHSOVVSTGYSRHVAVTVTRFLCGFLIPVFIITACYLTIVFKLORNRL
                                                                                                                                                                                                                                                                                                                                                                                   AKNKKPFKIIITIIITFFLCWCPYH-----TLYLLELHHTAVPSSVFSLGLPLATAVAI 304
                                                                                                                                                                                                                                                                                                                                                                                                          IKSSRPLRVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNP-TSSLAF
                                                                                                                                                                                                                                                                                                                                     FNSCLNPMLYVFVGQDFRERLIHSLPTSLERALSEDSAPTN 333
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0; Mismatches
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A;Molecule type: mRNA
A;Residues: 1-350 <BOU>
A;Residues: 1-350 <BOU>
A;Cross-references: UNIPROT:P21730; UNIPARC:UPI0000000C99; GB:J05327;
R;Gerard, N.P.; Gerard, C.
Rsture 349, 614-617, 1991
A;Title: The chemotactic receptor for human C5a anaphylatoxin.
A;Reference number: S13646; MUID:91156029; PMID:1847994
A;Accession: S13646
                                                                                                                                                                                                                                                    complement C5a anaphylatoxin receptor - human C;Species: Homo Bapiens (man) C;Date: 22-Jan-1993 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004 C;Date: 22-Jan-1993 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004 C;Accession: A37963; S13646; T52417; S30518 R;Boulay, F.; Mery, L.; Tardif, M.; Brouchon, L.; Vignais, P. Biochemistry 30, 2993-2999, 1991 Blochemistry 30, 2993-2999, 1991 A;Title: Expression cloning of a receptor for C5a anaphylatoxin on differen A;Reference number: A37963; MUID:91175748; PMID:2007135 A;Accession: A37963
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A;Residues: 1-473 <FUX>
A;Residues: 1-473 <FUX>
A;Residues: 1-473 <FUX
A;Cross-references: UNIPROT:O55197; UNIPARC:UPI0000126C12; GB:U86379; NID:g3015534; PIDN:
A;Experimental source: brain
C;Comment: This receptor plays a role in the central nervous systems.
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Keywords: glycoprotein; phosphoprotein
F;22-51/Domain: transmembrane #status predicted <TM1>
F;58-83/Domain: transmembrane #status predicted <TM1>
F;58-83/Domain: transmembrane #status predicted <TM2>
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F;322-347/Domain: transmembrane #status predicted <TM5>
F;326-347/Domain: transmembrane #status predicted <TM6>
F;367-392/Domain: transmembrane #status predicted <TM7>
F;406-430/Domain: transmembrane #status predicted <TM7>
F;9,201/Binding site: carbohydrate (Asn) (covalent) #status predicted F;360/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #
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Best Local S
Matches 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 ILPLVVLGVTFVLGVLGNGLVIMVAGFRMTRTVTTICYLNLALADFSFTATLFFLIVSMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PQVAIT-----ISRLVVGFLVPFFIMITCYSLIVFRMRKTNLTKSRNKTLRVAVAVVTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FFICWFPFQLVALLGTVW-----LKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPMLYVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----GGTPEERLK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSTGHVDDRTAPSSSVPARDLWTATTALQSQTFHTSPEDPFSQDSASQQPHYGGKPPTVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 161;
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A;Gene: GDB:CSR1; C5A; C5AR
A;Gross-references: GDB:128856; OMIM:113995
A;Map position: 19q13.3-19q13.4

• A;Introns: 1/3
A;Note: the list of introns may be incomplete
C;Function:
A;Description: mediates the inflammatory and chemotactic responses of poly
C;Superfamily: vertebrate rhodopsin
C;Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; inflamma
F;237-71/Domain: transmembrane #status predicted <TM1>
F;308-19/Domain: transmembrane #status predicted <TM2>
F;113-113/Domain: transmembrane #status predicted <TM5>
F;209-200-Domain: transmembrane #status predicted <TM6>
F;209-200-Domain: transmembrane #status predicted <TM7>
F;308-350/Domain: transmembrane #status predicted <TM6>
F;508-350/Domain: transmembrane #status predicted <TM7>
F;508-350/Domain: transmembrane #status predicted <TM6>
F;508-350/Domain: transmembrane #status predicted <TM7>
F;508-350/Domain: transmembrane #status predicted <TM7>
F;308-350/Domain: transmembrane #stat
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C;Genetics:
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342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 LLLATISADRFLLVFKPIWCQNFRGAGLAWIACAVAWGLALLLTIPSFLYRVV-----RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 FLIGFIALDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGD
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                                                                                                                DSLCVSFAYINCCINPITYVVAGQGFQGRLRKSLPSLLRNVLTEESVVRESKSFTRSTVD
                                                                                                                                                                       SSL----AFFNSCLNPMLYVFVGQDFRERLIHSLPTSLERALSEDSA-----PTND
                                                                                                                                                                                                                                 TWSRRATRSTKTLKVVVAVVASFFIFWLPYQVTGIM-----MSFLBPSSPTFLLLNKL
                                                                                                                                                                                                                                                               EYFPPKVLCGVDYSH-----DKRRERAV-----AIVRLVLGFLWPLLTLTICYTFILLR
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RESULT 9

865766

G protein-coupled receptor (clone AZ3B) - human

G;Species: Homo sapiens (man)

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997;

C;Accession: S65766

C;Acc
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A;Molecule type: mRNA
A;Residues: 1-482 <ROG>
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A;Title: cDNA cloning of a novel G protein-coupled receptor with a large extracellular load, Reference number: S65766; MUID:96180983; PMID:8605247
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A; Molecule type: mRNA A; Residues: 1-371 < OWM>

A;Cross-references: UNIPROT:O35786; UNIPARC:UPI0000127BD5; DDBJ:AJ002745; NID:g2624397;

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A;Experimental source: liver
C;Comment: This protein regulates the trafficking of immune of C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Keywords: glycoprotein; receptor; transmembrane protein
F;39-62/Domain: transmembrane #status predicted <TM2>
F;74-94/Domain: transmembrane #status predicted <TM3>
F;112-135/Domain: transmembrane #status predicted <TM4>
F;115-177/Domain: transmembrane #status predicted <TM4>
F;206-237/Domain: transmembrane #status predicted <TM6>
F;259-280/Domain: transmembrane #status predicted <TM6>
F;302-317/Domain: transmembrane #status predicted <TM7>
F;70.190/Binding site: carbohydrate (Asn) (covalent) #status I
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JC2492

G protein-coupled receptor 1 - rat

G protein-coupled receptor 1 - rat

N,Alternate names: GPR-1

C;Species: Rattus norvegicus (Norway rat)

C;Species: Rattus norvegicus (Norway rat)

C;Bate: 16-Mar-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004

C;Accession: JC2492

C;Accession: JC2492

R;Marchese, A.; Cheng, R.; Lee, M.C.; Porter, C.A.; Heiber, M.; Goodman, M.; George, S.;

R;Marchese, A.; Cheng, R.; Lee, M.C.; Porter, C.A.; Heiber, M.; Goodman, M.; George, S.;
                                                                                                                                                                                                                                                                                                                    A/Cross-references: UNIPROT:P46090; UNIPARC:UPI000012BA30; GB:S74702; NID:g786483; C/Superfamily: vertebrate rhodopsin C;Keywords: glycoprotein, lipoprotein; phosphoprotein; receptor; thiolester bond; t F;74-94/Domain: transmembrane #status predicted <TM2>.
F]112-133/Domain: transmembrane #status predicted <TM3>
                                                                                                                               F:134-135/Region: DR motif
F;155-175/Domain: transmembrane #status predicted <TM4>
F;155-29/Domain: transmembrane #status predicted <TM5>
F;209-229/Domain: transmembrane #status predicted <TM6>
F;246-266/Domain: transmembrane #status predicted <TM7>
F;245-306/Domain: transmembrane #status predicted <TM7>
F;245-306/Domain: transmembrane #status predicted <TM7>
F;245-306/Domain: transmembrane #status predicted <TM7>
F;251-306/Domain: transmembrane #status predicted <TM7>
F;150,231/Binding site: phosphate (Thr) (covalent) (by protein kinase #status predicted <TM7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 205, 1952-1958, 1994
A;Title: Mapping studies of two G protein-coupled receptor
A;Reference number: JC2492; MUID:95110347; PMID:7811287
A;Accession: JC2492
A;Molecule type: mRNA
A;Residues: 1-353 <MAR>
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Best Local S
Matches 120
                                                                                                           ;330/Binding site: palmitate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 --AAPEPFSHSTHPRTDPVGYSRHVAVT-----VTRFLCGFLIPVFIITACYLTIVFKL
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                                                                                                        (Cys)
Score 502; DB
Pred. No. 1.2e
72; Mismatches
                                                                                                              (covalent)
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n C;Superfamily: vertebrate rhodopsin C;Superfamily: vertebrate rhodopsin C;Keywords: chemotaxis; G protein-coupled receptor; glycoprot F;1-38/Domain: extracellular #status predicted <TM1>F;39-62/Domain: transmembrane #status predicted <TM1>F;39-62/Domain: transmembrane #status predicted <TM2>F;39-95/Domain: extracellular #status predicted <TM2>F;63-72/Domain: transmembrane #status predicted <TM2>F;96-111/Domain: extracellular #status predicted <TM3>F;112-133/Domain: intracellular #status predicted <TM3>F;134-150/Domain: intracellular #status predicted <TM5>F;151-175/Domain: transmembrane #status predicted <TM5>F;151-175/Domain: transmembrane #status predicted <TM5>F;209-229/Domain: transmembrane #status predicted <TM5>F;230-244/Domain: intracellular #status predicted <TM6>F;267-285/Domain: extracellular #status predicted <TM6>F;267-285/Domain: transmembrane #status predicted <TM7>F;286-309/Domain: transmembrane #status predicted <TM9>F;286-309/Domain: transmembrane #status predicted <T
                                                                                                                                                                                                                                                                                                                                             F;230-244/Do
F;245-266/Do
F;267-285/Do
F;266-309/Do
F;310-352/Do
F;5/Binding
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A;Residues: 1-352 <PER>
A;Cross-references: UNIPROT:P30992; UNIPARC:UPI0000126C87; EMBL:X65860; NID:g878; PIDN:CF
C;Function:
A;Description: mediates the inflammatory and chemotactic responses of polymorphonuclear r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 NYSYALEYYSQEPDAEENVYPGIVHWISLLLYALAFVLGIPGNAIVIWFMGFKWKKTVTT
                                                                                                     σı
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                                                                                                                                                                                                                                                        Similarity
FRMTRTVTTICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGS
                                                                                              NESPPEYPDYGTATLDENIFYDESLNTEKLSVPDMIALVIFYMVELVGVPGNFLVVWVTG
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                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                        27.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein-coupled receptor; glycoprotein; inflammation;
                                                                                                                                                         -LNEYEEVSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAG
                                                                                                                                                                                                                       Pred. No. 1.70
5; Mismatches
                                                                                                                                                                                                                                                        Score 500; DB 1;
Pred. No. 1.7e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-Sep-1999 #text_change
                                                                                                                                                                                                                                                                                  DB 1; Length 352;
                                                                                                                                                                                                                                                                                                                                                    #status
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RESULT 13
A55733
G protein-coupled receptor GPR1 - human
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A55733
R;Marchese, A.; Docharty, J.M.; Nguyen, T.; Heiber, M.; Cheng, R.; Heng, H.H.Q.; Tsui, I
Genomics 23, 609-618, 1994
A;Title: Cloning of human genes encoding novel G protein-coupled receptors.
A;Reference number: A55733
A;Reference number: A55733
A;Residues: preliminary
A;Maccession: A55733
A;Status: preliminary
A;Mesidues: 1-355 <MAR>
A;Residues: 1-355 <MAR>
A;Cross-references: UNIPROT:P46091; UNIPARC:UPI0000039D69; GB:U13666; NID:g577412; PIDN:
C;Genetics:
A;Gene: GDB:GPR1
A;Cross-references: GDB:371707; OMIM:600239
A;Map position: 15q25-15q26.1
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor
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Best Local Similarity
                                                                                                                                                                               181 F-NNHTLCYNNF-----QKHDPDLTLIRHHVLTWVKFIIGYLFPLLTMSICYLCLIF
                                                                                                                                                                                                                            169 IPNGDTYCTFNFASWGGTPEERLKVAITMLTARGI--IRFVIGFSLFMSIVAICYGLIAA 226
                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                  109 LFGSVFLIGFIALDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349 S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 WSRKATRSTKTLKVVVAVVVSFFVLMLPYQVTGMMMALFYKHSESFRRVSRLDSL---CV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 NGDTYCTFNFASWGGTPEERLKVAITMLTARG--IIRFVIGFSLPMSIVAICYGLIAAKI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 ILLLTTISADRFVLVFNPIWCQNYRGPQLAWAACSVAWAVALLLTVPSFIFRGVHTEYFP
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                                          285 NPTSSLAFFNSCLNPMLYVFVGQDFRERLIHSLPTSLERALSEDS 329
                                                                                                                                                                                                                                                                                                                                                               61 WFTGLKWKKTVTTLWFLNLAIADFIFLLFLPLYISYVAMNFHWPFGIWLCKANSFTAQLN
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                                                                                                                                                                                                                                                                        MFASVFFLTVISLDHYİHLIHPVLSHRHRTLKNSLIVIIFIWLLASLIGGPALYFRDTVE
                                                                                                                                                                                                                                                                                                                                                                                        WVAGFRMTRTVTTICYLNLALADFSFTATLFFLIVSMAMGEKWFFGWFLCKLIHIVVDIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HKKGMIKSSRPLRVLTAVVASFPICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FWMT-CGVDYSGVG-----VLVERGVAILRLLMGFLGPLVILSICYTFLLIRT
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  PLSTGLAPLNSCLNPILYVLISKKFQARFRSSVABILKYTLWBVS
                                                                                                                                   KIHKKGMIKSSRPLRVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYK--IIDILV 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLEETLFEEFENYSYDLDYYSLESDLEEKVQLGVVHWVSLVLYCLAFVLGIPGNAIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METNIFSTPLNEYEEVSYESAGYT------VLRILPLVVLGVTFVLGVLGNGLVI
                                                                                           KVKKKTVLISSRHFWTILVVVVAFVVCWTPYHLF----SIW-ELTIHHNSYSHHVMQAGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.5%; Score 499; DB 2; Length 355; 33.3%; Pred. No. 2.1e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30;
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RESULT 15 JC2134

angiotensin II receptor type 1A - N; Alternate names: AT1a receptor;

rat AT3

receptor

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F;111-132/Domain: transmembrane #status predicted <TM3>
F;133-149/Domain: intracellular #status predicted <TN4>
F;150-174/Domain: transmembrane #status predicted <TM4>
F;155-207/Domain: extracellular #status predicted <EX3>
F;208-228/Domain: transmembrane #status predicted <EX3>
F;208-224/Domain: intracellular #status predicted <TM5>
F;229-243/Domain: intracellular #status predicted <TM5>
F;244-265/Domain: transmembrane #status predicted <TM5>
F;246-284/Domain: extracellular #status predicted <TM6>
F;265-284/Domain: transmembrane #status predicted <TM7>
F;309-351/Domain: transmembrane #status predicted <TM7>
F;309-351/Domain: intracellular #status predicted <IN4>
F;6/Binding site: carbohydrate (Asn) (covalent) #status predicted <IN4>
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C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; inflammation; polymorph
F;1-37/Domain: extracellular #status predicted <EXI>
F;38-61/Domain: transmembrane #status predicted <INI>
F;38-71/Domain: intracellular #status predicted <INI>
F;72-94/Domain: transmembrane #status predicted <TW2>
F;72-94/Domain: transmembrane #status predicted <TW2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPARC:UPI00001637E6; GB:S46665; GB:L05630; NID:g257519; PIDN:AAB97; A;Experimental source: BALB/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-351 <GER>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                            326
                                                                                                                        267
                                                                                                                                                                                 266
                                                                                                                                                                                                                                             208
                                                                                                                                                                                                                                                                                                         206
                                                                                                                                                                                                                                                                                                                                                                  158 GVAWVLALLLTIPSFVYREAYKDFYSEHTVCGINYGG-GSFPKEK------AVAILR
                                                                                                                                                                                                                                                                                                                                                                                                                           147 VGPWILALVLTLPVFLFLTTV-TIPNGDTYCTFNFASWGGTPEERLKVAITMLTARGIIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 VAALIIYSVVFLVGVPGNALVVWVTAFEPDGPSNAIWFLNLAVADLLSCLAMPVLFTTVL
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                                                                                                                                                                              VWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPMLYVFVGQDFRERLIHSLPTSLERAL
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                                                            SEDSA-----PTNDTAANSA 340
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   SEDSVGRDSKTFTPSTDDTSTRKS
                                                                                                                     AWLPPS--SPTLKRVEKLNSLCVSLAYINCCVNPIIYVMAGQGFHGRLLRSLPSIIRNAL
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A;Status: preliminally
A;Molecule type: mRNA
A;Rosidues: 1-359 < max.
A;Rosidues: 1-359 < max.
A;Cross-references: UNIPARC:UPI0000125692
R;Cross-references: UNIPARC:UPI0000125692
R;Wai, N.; Yamano, Y.; Chaki, S.; Konlehi, P.; Bardhan, S.; Tibbetts, C.; Sasaki, K.; H
Biochem. Biophys. Res. Commun. 177, 299-304, 1991
A;Title: Rat angiotensin II receptor: cDNA sequence and regulation of the gene expressic
A;Reference number: JQ1055
A;Rolecule type: mRNA
A;Residues: 1-80, 'C', 82-108, 'T', 110-359 < max.
A;Rolecule type: mRNA
A;Residues: 1-80, 'C', 82-108, 'T', 110-359 < max.
A;Rolecule type: mRNA
A;Residues: 1-80, 'C', 82-108, 'T', 110-359 < max.
A;Rolecule type: mRNA
A;Residues: 1-80, 'C', 82-108, 'T', 110-359 < max.
A;Rolecule type: mRNA
A;Residues: 1-80, 'C', 82-108, 'T', 110-359 < max.
A;Rolecule type: mRNA
A;Residues: 1-80, 'C', 82-108, 'T', 110-359 < max.
A;Rolecule type: mRNA
A;Residues: 1-80, 'C', 82-108, 'T', 110-359 < max.
A;Rolecule type: mRNA
A;Residues: 1-80, 'C', 82-108, 'T', 110-359 < max.
A;Rolecule type: mRNA
A;Residues: 1-80, 'C', 82-108, 'T', 110-359 < max.
A;Residues: 1-80, 'C', 82-108, 'T', 11
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FEBS Lett. 298, 257-260, 1992
A;Title: Identification of two subtypes in the rat type I angiotensin II receptor.
A;Reference number: S20423; MUID:92183879; PMID:1544458
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A;Molecule type: mRNA
A;Residues: 1-359 CCON>
A;Cross-references: UNIPROT:P25095; UNIPARC:UPI0000125692
A;Cross-references: UNIPROT:P25095; UNIPARC:UPI0000125692
A;Note: the amino acid sequence of this protein is not given the amino acid sequence of this protein is not given the amino acid sequence of this protein is not given the amino acid sequence of this protein is not given the amino acid sequence of this protein is not given the amino acid sequence of this protein is not given the amino acid sequence of this protein is not given the amino acid sequence of this protein is not given the amino acid sequence of this protein is not given the amino acid sequence of this protein is not given the amino acid sequence of this protein is not given the amino acid sequence of this protein is not given the amino acid sequence of this protein is not given the amino acid sequence of this protein is not given the amino acid sequence of this protein is not given the amino acid sequence of this protein is not given the amino acid sequence of this protein is not given the amino acid sequence of this protein is not given the amino acid sequence of this protein is not given the amino acid sequence of this protein is not given the acid sequence of this protein is not given the acid sequence of the acid sequence of this protein is not given the acid sequence of the acid 
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C;Date: 28-Aug-1985 #sequence revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: JC2134; 815404; S20424; JQ1055
R;Conchon, S.; Monnot, C.; Sirieix, M.E.; Bihoreau, C.; Corvol, P.; Clauser, E.
Biochem. Biophys. Res. Commun. 199, 1347-1354, 1994
A;Title: Synthetic cDNA encoding the rat ATla reeptor: a useful tool for structure-fund A;Reference number: JC2134; MUID:94197726; PMID:8147879
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A;Accession: S15404
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A;Residues: 1-359 <MUR>
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Matches 105; Conserv
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                                                                                                                         268 LKEMLFYGKYK-IIDILVNPTSSLAFFNSCLNPMLYVFVGQDFRE---RLIHSLP---- 318
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Pred. No. 1.2e-28;
7; Mismatches 128;
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re greater than or equal to the score of the result being printed,
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1: uniprot_sprot:*
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P25090;
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Result

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Score

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Minimum Maximum

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Post-processing:

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Scoring table:

Title: Perfect score:

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9

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548.5 30.2 475 1 CJAR_CAVPO 543.5 29.9 356 2 QGNWS5 HUMAN 542.5 29.9 477 1 CJAR_MOUSE 542.5 29.9 477 2 QBC6R2_MOUSE 541.5 29.8 477 2 QBC6R2_MOUSE 531.5 29.6 371 1 CML1_MOUSE 531.5 29.4 371 2 QBU0HO HUMAN 531.5 29.4 371 2 QBU0HO HUMAN 531.5 29.4 371 1 CML1_HUMAN 531.5 29.2 382 1 GPR44_MOUSE 530.5 29.2 382 1 GPR44_MOUSE 530.5 29.2 382 2 QS4A00_MOUSE 530.5 29.2 382 1 GJAR_RAT 531.5 29.2 382 1 CJAR_HUMAN 509.5 28.0 482 1 CJAR_HUMAN	30.2 475 29.9 376 2 29.9 477 2 29.9 477 2 29.8 477 2 29.6 371 2 29.4 371 2 29.2 382 2 29.2 382 2 29.2 383 2 29.2 473 1 28.0 483 2 28.0 483 2	
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	088680 Q6nws5 Q09047 Q507a4 Q8c6r2 P97468 Q5u0h0 Q99736 Q92736 Q54800 Q54800 Q55197 P21730 Q16581 Q6xkd3	Q6XKD3_RAT

## ALIGNMENTS

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Ol-WAY-1992 (Rel. 22, Created)
Ol-JUL-1993 (Rel. 26, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
FMLP-related receptor I (FMLP-R-I) (Lipoxin A4 receptor) (LXA4
receptor) (Formyl peptide receptor-like 1) (RFP) (HM63).
Mame=FPRL1; Synonyms=FPR2, FPRH1, LXA4R;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Primates; Catarrhini; Hominidae;
TISSUE=Monocyte;
MEDLINE=94092629; PubMed=7505609;
Nomura H., Nielsen B.W., Matsushima K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Granulocyte;
MEDLINE=92246937; PubMed=1374236;
MEDLINE=92246937; PubMed=1374236;
Ye R.D., Cavanagh S.L., Quehenberger O., Prossnitz E.R.,
Cochrane C.G.;
"Isolation of a cDNA that encodes a novel granulocyte N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Bone marrow;
MEDLINE=92380523; PubMed=1511907; DOI=10.1016/0378-1119(92)90208-7;
Perez H.D., Holmes R., Kelly B., McClary J., Andrews W.H.;
Perez H.D., Holmes R., Kelly B., ecclary J., Andrews W.H.;
Perez H.D., Holmes R., Kelly B., McClary J., Andrews W.H.;
Perez H.D., Holmes R., Kelly B., McClary J., Andrews W.H.;
Perez H.D., Andrews W.H.;
Perez 
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MEDLINE=92307681; PubMed=1612600;

BEDLINE=92307681; PubMed=1612600;

Bao L., Gerard N.P., Eddy R.L. Jr., Shows T.B., Gerard C.;

"Mapping of genes for the human C5a receptor (C5AR), human FMLP receptor (FPR), and two FMLP receptor homologue orphan receptors (FPRH1, FPRH2) to chromosome 19.";

Genomics 13:437-440(1992).
                                                                                                                                                                                                                                                                                                                                                                                             Characterization and chromosome mapping receptor family.";
J. Biol. Chem. 267:7637-7643(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A structural homologue of the N-formyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
MEDLINE=92218423; PubMed=1373134;
Murphy P.M., Ozcelik T., Kenney R
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Balkesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Balkesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Balkesley R.W., Touchman J.W., Schmutz J., Myers R.M.,
"Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.",
Internation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RA Grimwood J., Gordon LA., Olsen A.S., Terry A., Schmutz J.,
RA Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,
RA Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,
RA Caenepeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M.,
RA Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Detter J.C.,
RA Escobar J., Flowers D., Fotopulos D., Garcia C., Georgescu A.M.,
RA Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,
RA Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,
RA Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,
RA Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,
RA Malfanti S., Martinez D., McCready P.M., Medina C., Morgan J.,
RA Nolson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,
RA Nolson K., Nolan M., Ovcharenko I., Fitluck S., Pollard M.,
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
RA Purey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,
Pennacchio L. A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
RA Rubin R M., Lucas S M..
                                                     TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rubin E.M., Lucas S.M.; "The DNA sequence and biology of Nature 428:529-535(2004).
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KODATZ S.A., Aronstam R.S., Sharma S.V.;
"cDNA clones of human proteins involved in sig
sequenced by the Guthrie cDNA resource center
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ
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  MEDLINE=97296322;
Takano T., Fiore
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Serhan C.N.,
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  PubMed=9151906;
S., Maddox J.F.,
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  DOI=10.1084/jem.185
Brady H.R., Petasis
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3 N.A.,
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PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

Chemotaxis; G-proteIn coupled receptor; Glycoprotein; Receptor; Sensory transduction; Transducer; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Expressed abundantly in the lung and
neutrophils. Also found in the spleen and testis.
SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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Bukaryota; Metazoa; Chordata; Craniata; Primates; Catarrhini; Hominidae;
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15-JUL-1998 (Rel. 36, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
PMLP-related receptor I (FMLP-R-I) (Fragment)
                   InterPro; IPR000826; Frt/met_receptor InterPro; IPR000276; GPCR_Rhodpsn. Pfam; PF00001; 7tm_1; 1.
                                                                                                     EMBL; X97739; CAA66323.1; -; HSSP; P34996; 1DDD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96421539; PubMed=8824156; DOI=10.1007/8002510050151; Alvarez V., Coto B., Sehen F., Gouzalek-Koces S., Lopez-Larrea C.; "Molecular evolution of the N-formyl peptide and C5a receptors in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenetics 44:446-452(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human primates."
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                                                                                                                                                                                                                                    B Swiss-Prot entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                WINCTION: Low affinity receptor to N-formyl-methionyl peptides, which are powerful neutrophils chemotactic factors. Binding of PMLP to the receptor causes activation of neutrophils. This response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. SUBCELLULAR LOCATION: Integral membrane protein.
SUBCELLULAR LOCATION: The grant membrane protein.
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PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G-PROTEIN RECEP_F1_2; 1.

Chemotaxis; G-protein coupled receptor; Glycoprotein; Receptor; Sensory transduction; Transducer; Transmembrane.
                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
FMLP-related receptor I (FMLP-R-I) (Fragment)
NUCLEOTIDE SEQUENCE.
MEDLINE=96421539; PubMed=8824156; DOI=10.1007/s002510050151;
Alvarez V., Coto E., Sehen F., Gouzalek-Koces S., Lopez-Larr
                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                   Gorilla gorilla gorilla (Lowland gorilla).
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Cytoplasmic (Potential).
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Extracellular (Potential).
7 (Potential).
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Pred. No. 1.9e-98
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

Chemotaxie; G-protein coupled receptor; Glycoprotein; Receptor; Sensory transduction; Transducer; Transmembrane.
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PRINTS; PR00526; FMETLEUPHER.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1_1;

PROSITE; PS50262; G PROTEIN RECEP F1_2;
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SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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PROSITE; PS00237; G_PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
Chemotaxis; G-protein coupled receptor; Glycoprotein; Receptor; Sensory transduction; Transducer; Transmembrane.
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InterPro; IPR000826; Prt/met_receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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15-JUL-1998 (Rel. 36, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
FMLP-related receptor I (FMLP-R-I) (Fragment)
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InterPro; IPR000276; Frt/met receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00526; FMETILEUPHER.
PRINTS; PR005237; GPCRRHODOPSN.
PROSITE; PS00237; GPCRRHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS002637; GPROTEIN RECEP F1 2; 1.
Chemotaxis; G-proteIn coupled receptor; Glycoprotein; Receptor; Sensory transduction; Transducer; Transmembrane.
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                                                                                                                                                                                                                                                                                    s Swiss-Prot entry is copyright. It is produced through a collable ween the Swiss Institute of Bioinformatics and the EMBL outsi European Bioinformatics Institute. There are no restrictions as long as its content is in no way modified and the strictions.
                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Low affinity receptor to N-formyl-methionyl peptides, which are powerful neutrophils chemotactic factors. Binding of PMLP to the receptor causes activation of neutrophils. This response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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(Rel. 47,
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Last annotation update)
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    NUCLEOTIDE SEQUENCE.

MEDLINE=98390190; PubMed=9722950; DOI=10.1006/geno.1998.5376; Gao J.-L., Chen H., Filie J.D., Kozak C.A., Murphy P.M.;

"Differential expansion of the N-formylpeptide receptor gene c in human and mouse.";

Genomics 51:270-276(1998).
                                                                                                                                                                         Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Eua
Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
N-formylpeptide receptor-like 2 (Lipoxin A4 receptor-like
                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                        Name=Fpr-rs2;
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1 (Potential).

Cytoplasmic (Potential).

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Extracellular (Potential).

3 (Potential).
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Cytoplasmic (Potential).
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Potential.
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Pred. No. 6
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oglires; Glires; Rodentia; Sciurogna
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Matches 267
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RGO; GO:0004872; F:receptor activity; IDA.

InterPro; IPR001644; C3Aantx_receptor.

InterPro; IPR000826; Frr/met_receptor.

InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm 1; 1.

PFINTS; PR01060; C3ANPHYLTXNR.

PRINTS; PR01060; C3ANPHYLTXNR.

PRINTS; PR00237; GPCRRHODOPSN.

R PROSITE; PR00237; GPCRRHODOPSN.

R PROSITE; PS00237; GPCRTEIN_RECEP_F1_1; UNKNOWN_1.

R PROSITE; PS00237; GPCRTEIN_RECEP_F1_2; 1.
                                                                                                                                                   FPRLI_MOUSE STANDARD,

O08790;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation deate)
NUCLEOTIDE SEQUENCE.
TISSUE-Neutrophil, and Spleen;
MEDLINE=97296322; PubMed=9151906;
MEDLINE=97296322; Maddox J.F.,
                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor.
SEQUENCE
                                                                      NCBI_TaxID=10090;
                                                                                                                                          Name=Fprl1; Synonyms=Lxa4r;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vaughn M.W., Proske R.J., Haviland D.L.;
"Identification, cloning, and functional ch
lipoxin A4 receptor homologue gene.";
J. Immunol. 169:3363-3369(2002)
EMBL; AP071180; AAC34585.1; -; Genomic_DNA.
EMBL; AY138248; AAN06932.1; -; Genomic_DNA.
EMBL; AY138248; AAN06922.70; Mus musculus.
                                                                                                                                                                                                                                                      MOUSE
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267; Conserv
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                                                                                                                                                                                                                                                                                                          LYVFMGQDFRERPIHSLPYSLERALSEDSGQTSDSSTSSTSPPADIELKA
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Pred. No. 6.6e-77;
3; Mismatches 50
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       DOI=10.1084/jem.185.
Brady H.R., Petasis
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PRINTS; PRO1060; CJANPHYLTXNR.
PRINTS; PRO10526; FMETLEUPHER.
PRINTS; PRO0237; GPCREHODDESN.
PROSITE; PS00237; GPCREHODDESN.
PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
Chemotaxis; G-protein coupled receptor; Glycoprotein; Receptor; Chemotaxis; G-protein coupled receptor; Grandware.
Sensory transduction; Transducer; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serhan C.N.;

"Aspirin-triggered 15-epi-lipoxin A4 (LXA4) and LXA4 stable analogues are potent inhibitors of acute inflammation: evidence for anti-inflammatory receptors.";

J. Exp. Med. 185:1693-1704(1997).

-I-FUNCTION: Low affinity receptor to N-formyl-methionyl peptides, which are powerful neutrophils chemotactic factors. Binding of FMLP to the receptor causes activation of neutrophils. This response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. The activation of LXA4R could result in an anti-inflammatory outcome counteracting the actions of proinflammatory signals such as LTB4
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GO; GO:0006335; P:chemoteaxis; TAS.
GO; GO:0007186; P:G-protein coupled receptor
InterPro; IPR001644; C3Aantx_receptor.
InterPro; IPR000826; Prt/met receptor.
InterPro; IPR000876; GPRR, Rhodpsn.
Pfam; PF00001; 7tm.1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (leukotriene B4).

I SUBCELULAR LOCATION: Integral membrane protein.

I SUBCELULAR LOCATION: Integral membrane protein.

I TISSUE SPECIFICITY: Expressed mostly in neutrophils, followed by spleen and lung. Expressed at very low levels in heart and lively spleen and lung. Expressed at very low levels in heart and lively spleen and lung. Expressed at very low levels in heart and lively.

SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U78299; AAC53198.1; -; mRNA.
Ensembl; ENSMUSG00000052270; Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its tuse as long as its content is in no way modified and this statement is not
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13
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257; Conser
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            TICYLNLALADPSFTATLPFLIVSMAMGEKWPPGWFLCKLIHIVVDINLFGSVFLIGFIA
                                                                          METNESTPLNEYEEVSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVT
 TIWYLNLALADFSFTATLPFLLVEMAMKEKWPFGWFLCKLVHIAVDVNLFGSVFLIAVIA
                                                          MESNYSIHLINGSEVVVYDSTISRVLWILSMVVVSITFFLGVLGNGLVIWVAGFRMPHTVT
                                                                                                                                                                                                Conservative
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                                                                                                                                    73.6%;
73.2%;
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                                                                                                                                                                                                                                                      Cytoplasmic (Potential).
2 (Potential).
Extracellular (Potential).
3 (Potential).
4 (Potential).
4 (Potential).
5 (Potential).
Extracellular (Potential).
Cytoplasmic (Potential).
5 (Potential).
Cytoplasmic (Potential).
6 (Potential).
7 (Potential).
Extracellular (Potential).
7 (Potential).
                                                                                                                     29;
                                                                                                                    Score 1337; DB 1;
Pred. No. 5.7e-72;
9; Mismatches 65
                                                                                                                                                                               Cytoplasmic (Potential).

-linked (GlcNAc. . .) (Potential)

N-linked (GlcNAc. . .) (Potential)

Potential.

1AF3B374B195B0CB CRC64;
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A Strausberg R.L., Pedingold E.A., Grouse L.H., Derge J.G.,

Kilausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan K., Farmer A.A., Rubin G.M., Hong L.,

A Hopkins R.F., Jordan K., Farmer A.A., Rubin G.M., Hong L.,

A Hopkins R.F., Jordan K., Farmer A.A., Rubin G.M., Hong L.,

A Hopkins R.F., Jordan K., Farmer A.A., Rubin G.M., Hong L.,

A Hopkins R.F., Jordan K., Farmer A.A., Peters G.J., Ju, Scheetz T.E.,

A Hopkins R.F., Jordan R.J., Peters G.J., Abramson R.D., Mullahy S.J.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Sarcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Sarcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Sarcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Sarcia A.M., Gay L.J., Hulyk S.W.,

A Rahey J., Haldon A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Hopkins R.F., Jones S.J.M., Marra M.A.;

A Hopkins R.F., Jones S.J.M., Marra M.A.;
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FPRL2 HI
P25089;
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MEDLINE=94256976; PubMed=8198572;
Durstin M., Gao J.-L., Tiffany H.L., McDermott D., Murphy P.M.;
"Differential expression of members of the N-formylpeptide receptor gene cluster in human phagocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-MAR-2004 (Rel. 43, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
FMLP-related receptor II (FMLP-R-II) (Formylpeptide receptor-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
KOPATZ S.A., Aronstam R.S., Sharma S.V.;
"CDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bao L., Gerard N.P., Eddy R.I. "Mapping of genes for the hum receptor (FPR), and two FMLP (FPRHI, FPRH2) to chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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MEDLINE=92307681; P
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(Rel. 43,
(Rel. 47,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ
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Best Local S
Matches 255
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GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0005882; F:N-formyl peptide recept
GO; GO:0006928; P:cell motility; TAS.
GO; GO:0007165; P:signal transduction; TY
InterPro; IPR000276; GFCR_Rhodpsn.
InterPro; IPR000276; GFCR_Rhodpsn.
                                                                     CONFLICT
CONFLICT
SEQUENCE
                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                TRANSMEM TOPO_DOM
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EMBL;
                                                                                                                                                                                                                                                                                      TRANSMEM TOPO_DOM
                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00526; FMETLEUPHER.
PRINTS; PR00237; GPCRHODODSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

Chemotaxis; G-protein coupled receptor; Glycoprotein; Receptor; Sensory transduction; Transducer; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00001; 7tm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; C42009; C42009.
Ensembl; ENSG00000187474; Homo sapiens.
                                                                                                                            CARBOHYD
                                                                                                                                                              TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
c. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
prince in the seceptor to N-formyl-methionyl peptides, which are powerful neutrophils chemotactic factors. Binding of PMLP to the receptor causes activation of neutrophils. This response is mediated via a G-protein that activates a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphatidylinositol-calcium second messenger system.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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                                    Similarity
METNFSTPLNBYBBVSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVT
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51
62
84
101
122
                                                                   AAH69593.1; -;
AAH69812.1; -;
                                  73.0%;
72.2%;
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                          38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to membrane;
                         Score 1327; I
Pred. No. 2.3e
88; Mismatches
                                                                                                                          Cytoplasmic
N-linked (G1
N-linked (G1
                                                                               Potential
G -> A (i)
S -> T (i)
D -> H (i)
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6 (Potential
Extracellula
7 (Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA.
                                                                                                                                                                                                        Extracellular (Potential).
5 (Potential).
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                                                                     3 -> A (in Ref. 1).
5 -> T (in Ref. 1).
) -> H (in Ref. 1).
FFB7150B6A833F4C
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nes 58;
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METNFS I PLNETEEVLPBPAGHTVLWI FSLLVHGVTFVFGVLGNGLVI WVAGFRMTRTVN

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RESULT 9
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Q615J4 HUMAN PRELIMINARY;
AC Q615J4;
AC Q615
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Best Local Similarity
Matches 255; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
Burkhart-Schultz K.J., Brower A., Gordon L., Dias J., Ramirez M.,
Stilwagen S., Phan H., Velasco N., Do L., Regala W., Terry A.,
Garnes J., Danganan L., Erler A., Christensen M., Georgescu A.,
Avila J., Liu S., Attix C., Andreise T., Trankheim M.,
Amico-Keller G., Coefield J., Duarte S., Lucas S., Bruce R.,
Thomas P., Quan G., Krommiller B., Arellano A., Sanders C., Ow D.,
Nolan M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.;
Submitted (NOV-1998) to the EMBL/GenBank/DDJ databases.
EMBL; AC005946; AAC72102.1; -, Genomic DNA.
SEQUENCE 353 AA; 3965 MW; FFB7150B6A833F4C CRC64;
301
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LYVFVGQDFRERLIHSLPTSLERALSE--DSAPTNDTAANSASPPAETELQAM
                                                 RVFAAVVASFFICWFPYELIGILMAVWLKEMLLNGKYKIILVLINPTSSLAFFNSCLNPI
                                                                             RVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.0%; Score 1327; DB 2; 72.2%; Pred. No. 2.3e-71;
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Matches 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REMBL; APO71179; AAC34584.1; -; Genomic DNA.

RENSembl; ENSMUSGO0000052270; Mus musculus.

RENSembl; ENSMUSGO0000052270; Mus musculus.

REGO; MGI:1278320; Fpr-rs1.

REGO; GO:0016021; C:integral to membrane; IEA.

REGO; GO:0004982; F:N-formyl peptide receptor activity; IEA.

REGO; GO:0004872; F:receptor activity; IEA.

REGO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

REGO; GO:0001584; F:Thodopsin-like receptor protein signal:

REGO; GO:0001186; F:G-protein coupled receptor protein signal:

REGO; GO:0001186; F:G-protein coupled receptor.

RINTEPRO; IPR000644; C3Aantx_receptor.

RINTEPRO; IPR000826; FT/met_receptor.

RETITEPRO; IPR000826; FT/met_receptor.

RETINTS; PR01060; C3ANPHYLTANR.

REPRINTS; PR01051; T-M=1; 1.

REFINTS; PR00237; GECRHODOPSN.

REFINTS; PR00237; GECRHODOPSN.

RECEPTOR:

REC
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01-NOV-1998 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor.
SEQUENCE
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in human and mouse.";
Genomics 51:270-276(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurogna
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-formylpeptide receptor-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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257; Conserv
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                        LYVFVGQDFRERLIHSLFTSLERALSEDSAFTNDTAANSASFPAETELQAM 351
                                                                                                                  RVLTAVVASFFICWFDFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPM
                                                                                                                                                                                                                    ASWGGTPBERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPL
                                                                                                                                                                                                                                                                                     LDRCICVLHPVWAQNHRTVSL----VVGSWIFALILTLPLFLFLTTVRDARGDVHCRLSF
                                                                                                                                                                                                                                                                                                              LDRCICVLHEVWAQNHRTVSLAMKVIVGEWILALVLTLEVELELTTVTIENGDTYCTENF 180
                                                                                                                                                                                                                                                                                                                                                                                 TIWYLNLALADESETATLEELLVEMAMKEKWEEGWELCKLVHIAVDVNLEGSVELIAVIA
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LYVFMGQDFQERLIHSLSSRLPRALSEDSGHISDTRTNLASLPEDIEIKAI
                                                                                         RVLTGVVASFFICWFPFQLVALLGTVWLKEMQFSGSYKIIGRLVNPTSSLAFFNSCLNPM
                                                                                                                                                                                        VSWGNSVEERLNTAITFVTTRGIIRFIVSFSLPMSFVAICYGLITYKIHKKAFVNSSRPS
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I., Filie J.D., Kozak C.A., Murphy P.M.;

mansion of the N-formylpeptide receptor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39071 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.9%; Score 1325; DB 2; Length 347; 73.2%; Pred. No. 2.9e-71; tive 27; Mismatches 63; Indels
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SOLD COUNTRY AND SERVICE OF THE SERV
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FPRL2_PANT
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Matches 252
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CARBOHYD
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PRINTS; PR00526; PMETLEUPHER.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

Chemotaxis; G-protein coupled receptor; G1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X97743; CAA66327.1; -; Genomic I
InterPro; IPR000826; Frt/met_receptor
InterPro; IPR000276; GPCR_Rhodpsn.
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15-JUL-1998 (Rel. 36,
10-MAY-2005 (Rel. 47,
FMLP-related receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96421539; PubMed=8824156; DOI=10.1007/8002510050151; Alvarez V., Coto E., Sehen F., Gouzalek-Koces S., Lopez-Larrea C.; "Molecular evolution of the N-formyl peptide and C5a receptors in non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=FPRL2;
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                      Similarity
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62
62
101
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141
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  Conservative
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121
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162
205
226
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                    72.2%;
72.2%;
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Last annotation
II (FMLP-R-II)
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                                                                                      MW;
  37;
Score 1312; DB 1;
Pred. No. 1.7e-70;
7; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                              Cytoplasmic (Potential).
2 (Potential).
Extracellular (Potential)
3 (Potential).
                                                                                                                                                                                                                         Extracellular (Potential).
7 (Potential)
                                                                                                                                                          N-linked
                                                                                                                                                                              N-linked
                                                                                                                                                                                                Cytoplasmic (Potential).
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(Formylpeptide receptor-like
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                                                                                                                                                   (GlcNAc. . .) (Potential). (GlcNAc. . .) (Potential).
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                                                                                                                                                                                                                                                                                      (Potential).
                                                                                                                                                                                                                                                                                                                                                                        (Potential).
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    Indels
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RESULT 12
PRESULT 12
PRESULT 197913
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TOPO_DOM
TOPO_DOM
TOPO_DOM
                                                                                      PRINTS; PR00526; FMETLEUPHER.
PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
Chemotaxis; G-protein coupled receptor; Glycoprotein; Receptor; Sensory transduction; Transducer; Transmembrane.
                                                                                                                                                                                                                                                                                      EMBL; X97741; CAA66325.1; -; Genomic_DNA.
InterPro; IPR000826; Frt/met_receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pongo pygmaeus (Orangutan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
PMLP-related receptor II (FMLP-R-II) (Formylpeptide receptor-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96421539; PubMed=8824156; DOI=10.1007/s002510050151; Alvarez V., Coto E., Sehen F., Gouzalek-Koces S., Lopez-Larrea "Molecular evolution of the N-formyl peptide and C5a receptors
                                                                                                                                                                                                                                                                    Pfam; PF00001; 7tm
                                                                                                                                                                                                                                                                                                                                                                                                                                      use as long as its content is in no way modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenetics 44:446-452(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Low affinity receptor to N-formyl-methionyl peptides, which are powerful neutrophils chemotactic factors. Binding of PMLP to the receptor causes activation of neutrophils. This response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute.
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RESULT 13
FPRL2 GORG
ID FPRL2
AC P7917
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GN Names
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OC Mamma
OC GOR1
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Best Local Similarity
Matches 250; Conserv
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FPRL2 GORGO
P79178;
15-JUL-1998
15-JUL-1998
10-MAY-2005
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MEDLINB=96421539; PubMed=882
Alvarez V., Coto E., Sehen F
"Molecular evolution of the
human primates.";
                                                                                                                                                                                                                                                        Gorilla gorilla (Lowland gorilla).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
Gorilla.
                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
FMLP-related receptor II (FMLP-R-II) (Formylpeptide receptor-like (Fragment).
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  Immunogenetics 44:446-452(1996).
-!- FUNCTION: Low affinity receptor to N-formyl-methionyl peptides,
-!- which are powerful neutrophils chemotactic factors. Binding of
FMLP to the receptor causes activation of neutrophils. This
response is mediated via a G-protein that activates a
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                                                                                                                            PubMed=8824156; DOI=10.1007/8002510050151;
E., Sehen F., Gouzalek-Koces S., Lopez-Larr
ion of the N-formyl peptide and C5a recepto
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Pred. No. 5.2e-70;
9; Mismatches 58
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Extracellular (Potential)

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-linked (GlCNAc. . .) (Potential).
N-linked (GlCNAc. . .) (Potential).
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Extracellular (Potential).
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C5a receptors
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PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; GPCOTEIN RECEP F1_1; 1.

PROSITE; PS50262; GPROTEIN RECEP F1_2; 1.

Chemotaxis; G-proteIn coupled receptor; Glycoprotein; Receptor; Sensory transduction; Transducer; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphatidylinositol-calcium second messenger system.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to the G-protein coupled receptor 1
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                                                               LYVFVGQDFRERLIHSLPTSLERALSE--DSAPTNDTAANSASPPAETE
                                                                                                   RVLTAVVASFFICWFFFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPM
                                                                                                                                  LDRCICVLHPAWAQNHRTMSLAKRVMTGLWILTIVLTLPNFIFWTTISTTNGDTYCIFNF
                                                                                                                                                                                    LDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNF
                                                                                                                                                                                                                 TICYLNLALADFSPSAILPFHMVSVAMREKWPFGSFLCKLVHVMIDINLFVSVYLITIIA
                                                                                                                                                                                                                           TICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIA 120
                                                                                                                                                                                                                                                                   METNESTPLNEYEEVSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAGERMTRTVT
                                                     LYVFLGSNFQERLIRSLPTSLERALTEVPDSAQTSNTHTTSASPPEETE
                                                                                                                                                                                                                                                       METNESIPLNETEEVLPEPAGHTVLWIFSLLVHGVTFIFGVLGNGLVIWVAGFLMTRTVN
                                                                                           RVFAAVVASFFICWFPYELIGILMAVWLKEMLLNGKYKIILVLINPTSSLAFFNSCLNPI
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                                                                                                                                                                                                                                                                                              Conservative
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Extracellular
3 (Potential)
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_receptor.
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N-linked (GlcNAc...) (Potential).
N-linked (GlcNAc...) (Potential).
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PRINTS; PR00526; PMCTLEUPHER.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X97740; CAA66324.1; -; Genomic_DNA.
InterPro; IPR000826; Frt/met_receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
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Bukaryota; Metazoa; Chordata; Caraniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Cercopithecidae; Cercopithecinae; Macaca.
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MEDLINE=96421539; Pu
                                                                                                                         SEQÜENCE
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                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Swiss-Prot entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bloinformatics Institute. There are no restrictions on its as long as its content is in no way modified and this statement is not
 13
                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                        transduction;
                                     METNFSTPLNEYBEVSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIMVAGFRMTRTVT
 TICYLNLALADFSFTATLFFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIA
                        METNFSIPLNETEEVLPEPAGHTVLWIFSLLVHGVTFIFGVLGNGLVIWVAGFRMTRTVN
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50262; G PROTEIN RECEPTOR; Glycoprotein; Receptor; G-protein coupled receptor; Glycoprotein; Receptor; nsduction; Transducer; Transmembrane.

27 Extracellular (Potential).
                                                                        Conservative
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z., Sehen F., Gouzalek-Koces S., Lopez-Larr
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II (FMLP-R-II) (Formylpeptide receptor-like
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5 (Potential) Cytoplasmic (Potential).
6 (Potential) Extracellular (Potential).
7 (Potential).
                                                                                   Score 1292; DB 1;
Pred. No. 2.7e-69;
                                                                                                                                                         Cytoplasmic (Potential).
N-linked (GlcNAc. . .) (
N-linked (GlcNAc. . .) (
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Murphy P.M., McDermott D.;
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Biochem. Biophys. Res. Commun. 168:1103-1109(1990).
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NUCLEOTIDE SEQUENCE.
MEDLINE=94040825; PubMed=8224916; DOI=10.1016/0378-1119(93)90653-K;
Murphy P.M., Tiffany H.L., McDermott D., Ahuja S.K.;
                                                                                                                 "Mapping of genes for the human C5a receptor (C5AR), human receptor (FPR), and two FMLP receptor homologue orphan rece (FPRH1, FPRH2) to chromosome 19.";
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Boulay F., Tardif M., Brouchon L., V
"The human N-formylpeptide receptor.
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Eukaryota; Metazoa; (
Mammalia; Eutheria; I
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                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                            MEDLINE=91286286; PubMed=1712023;
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RA Strauberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Expleton M., Soares M.B., Bonaldo M.F., Casvant T.L., Hong L.,
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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci R., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Vilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
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RI Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,

RA Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,

RA Caenepeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M.,

RA Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Detter J.C.,

RA Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,

RA Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,

RA Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,

RA Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,

RA Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J.,

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RA Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,

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RA Pursy T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,

Robin R M. Lincas S M. M.
Perez H.D., Holmes R., Kelly E. "Cloning of the gene coding for Characterization of a promoter
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Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein
Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kopatz S.A., Aronstam R.S., Sharma S.V., roDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org).", Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                            PubMed=1445895;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E.M., Lucas S.M.;
DNA sequence and biology
e 428:529-535(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3
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    Kelly E., McClary J., Chou Q., Andrews W.H.; oding for a human receptor for formyl peptides. promoter region and evidence for polymorphic
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DR GO; GO:0005768; C:endosome; TAS.

DR GO; GO:0005886; C:plasma membrane; TAS.

DR GO; GO:0005886; C:plasma membrane; TAS.

DR GO; GO:0004982; F:N-formyl peptide receptor activity; TAS.

DR GO; GO:0000187; F:receptor activity; TAS.

DR GO; GO:0000187; P:activation of MAPK; TAS.

DR GO; GO:0000187; P:activation of MAPK; TAS.

DR GO; GO:0000187; P:activation of MAPK; TAS.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.

DR GO; GO:0007186; P:G-protein signaling, coupled to cAMP nucleo. .; TAS.

DR GO; GO:0007186; P:G-protein signaling, coupled to cAMP nucleo. .; TAS.

DR GO; GO:0007186; P:frimet receptor.

DR GO; GO:0007186; P:signal transduction; TAS.

DR GO; GO:0007165; P:signal transduction; TAS.

DR GO; GO:0007263; P:STIZUUHER.

DR PROSITE; PRO00217; GPCRRHODOPS.

DR PROSITE; PS00237; GPCRRHODOPS.

DR PROSITE; PS00237; GPCRRHODES.

DR PROSITE; PS00237; GPCRRHODES.

DR PROSITE; PS00237; GPCRRHODES.

DR PROSITE; PS00237; GPCRRHODES.

Chemotaxis; G-protein coupled receptor; Glycoprotein; Phosphorylation;

Chemotaxis; G-protein coupled receptor; Glycoprotein; Phosphorylation;
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between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no the European Bioinformatics in no way modified and
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MEDLINE-99445530; PubMed=10514456; DOI=10.1074/jbc.274.42.29791;
Maestes D.C. Potter R.M., Prossnitz E.R.;
"Differential phosphorylation paradigms dictate desensitization and internalization of the N-formyl peptide receptor.";
J. Biol. Chem. 274:29791-29795(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ensembl; ENSG00000171051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This Swiss-Prot entry is copyright. It is produced through
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[12]
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11; M60626; AAA35846.1; -; mRNA.

3L; M60627; AAA35847.1; -; mRNA.

11; L10820; AAA16863.1; -; Unassigned DNA.

11; L10820; AAP58403.1; -; Genomic_DNA.

12; AY301273; AAP58403.1; -; mRNA.

13; BT007429; AAP36097.1; -; mRNA.

14; AC018755; AAF87842.1; -; Genomic_DNA.

15; BC005315; AAF05315.1; -; mRNA.

15; S49810; AAD14906.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        which are powerful neutrophils chemotactic factors. Binding FMLP to the receptor causes activation of neutrophils. This response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. SUBCELIULAR LOCATION: Integral membrane protein.

TISSUB SPECIFICITY: Neutrophils
TISSUB SPECIFICITY: Neutrophils
PTM: Phosphorylated; which is necessary for desensitization. SIMILARITY: Belongs to the G-protein coupled receptor 1 fami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: High affinity receptor for N-formyl-methionyl peptides, which are powerful neutrophils chemotactic factors. Binding of
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121 LDRCVCVLHEVWTQNHRTVSLAKKVIIGEWVWALLLTLEVIIRVTTVPGKTGTVACTENE	DЪ
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61 TISYLNLAVADPCFTSTLPFFMVRKAMGGHWPEGWFLCKFLFTIVDINLFGSVFLIALIA	ᇝ
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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

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3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

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US-08-118-270-34
US-08-118-270-34
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US-09-170-496D-270
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PCT-US93-08528-35
US-08-513-9748-350
US-08-513-9748-350
US-08-513-9748-350
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US-08-450-393A-8
US-08-393-508-5
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Sequence 2, Appli
Sequence 499, App
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Sequence 3, Appli
Sequence 10, Appli
Sequence 10, Appli
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Sequence 246, App
Sequence 246, App
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			Matches	S-09-944- S-09-944- S-09-944- S-09-941- GENERAL APPLICA TITLE 0 TITLE 0 TITLE 0 CURRENT CURRENT CURRENT PRIOR P NUMBER   SOFTWAR SEQ ID N LENGTH TYPE: ORGANI S-09-944-		0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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LYVFVGQDI	ASWGGTPEERLKVAITMLTARG	TICYLNLALADESETATLEEL LDRCICVLHEVWAQNHRTVSL	I; Conservative 0; Mismatches  METNFSTDLNEYEEVSYESAGYTVLRILDLVVLGVT	n NO 822		222222222222222222222222222222222222222
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APTNOT.	LPMS LPMS LFYG 	PFGW LALV	es VLGVT VLGVT	subs y con iseas	κi	US-08-446-669-8 US-09-625-573-8 PCT-US95-00476-8 US-08-458-970A-11 US-08-468-209A-4 US-09-867-915-3 US-09-949-016-7391 US-09-949-016-7315 US-09-949-016-7115 US-09-08-016-3784-46 US-09-08-378-46 US-09-08-378-46 US-09-08-378-46 US-08-08-08-378-46 US-08-08-08-08-08-08-08-08-08-08-08-08-08-
OTAANSASI           TAANSASI	IRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSS	.IVSMAMGEKMPFGWFLCKLIHIVVDINLEGSVFLIGFI AMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTEN	TFVLG	substances conditions seases		666 5711 888
2-2	ICYGLIAAKII	1474/      1874/ 1874/	0; Indels 0; Gaps  FVLGVLGNGLVIWVAGFRMTRTVT                       FVLGVLGNGLVIWVAGFRMTRTVT  CKLIHIVVDINLFGSVFLIGFIA	Leen v		
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	240 240 300 300	120 180 180	60 60 120			

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APPLICANT: Lihmann-Bruinsma, Karin
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I Lin
APPLICANT: Lin, I Lin
APPLICANT: Lin, I Lin
TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Know
TITLE OF INVENTION: Protein-Coupled Receptors
FILE REFERENCE: AREN-207
CURRENT APPLICATION NUMBER: US/09/826,509
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR APPLICATION STATE 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOPTWARE: Patentin Version 2.1
SEQ ID NO 501
LENGTH: 351
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US-09-826-509-501
; Sequence 501, Applicat
; Patent No. 6806054
; GENERAL INFORMATION:
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US-09-826-509-501
                                                                                                                                                                                                                                      Sequence 499, Application US/09826509
Patent No. 6806054
GENERAL INFORMATION:
APPLICANT: Lehmann-Bruinsma, Karin
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, I-Lin
                 TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known TITLE OF INVENTION: Protein-Coupled Receptors FILE REFERENCE: AREN-207
CURRENT APPLICATION NUMBER: US/09/826,509
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 1998-10-13
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NUMBER
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OF SEQ ID NOS: 589
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99.7%;
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Pred. No. 2.6e-126;
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RESULT 4
US-07-759-568-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Version SEQ ID NO 499 LENGTH: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Murphy, Philip M.
TITLE OF INVENTION: Cloning of cDNA Encoding a Functional
TITLE OF INVENTION: Human Interleukin-8 Receptor
NUMBER OF SEQUENCES: 5
             TELEX: 6714627 cush
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acid
                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Scott, Watson T.
REGISTRATION NUMBER: 26581
REFERENCE/DOCKET NUMBER: WTS/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 350
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                           C11.
STATE: USA
COUNTRY: USA
TTD: 20036-5601
TTD: TTDADABLE F
                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                         ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                               APPLICATION NUMBER: UPFILING DATE: 19910913
CLASSIFICATION: 435
                                                                                            TELEPHONE: 202-861-300
TELEFAX: 202-822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Cushman,
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I: 350 amino acids
AMINO ACID
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1615 L Street, N.W.
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                                                                                                                           PILING DATE: 28-APRILING DATE: 28-APRILING CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: ROBITSON, JOSEPH R.
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08430286A Patent No. 6225080 GENERAL INFORMATION:
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 240;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: lir
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, V. CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,286A
FILING DATE: 28-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Barby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Eppler, C. Mark
APPLICANT: Wang, Jai-Bel
TITLE OF INVENTION: Mu-Subtype Opioid Receptor
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 LYVFMGQDFRERLIHALPASLERALTEDSTQTSDTATNSTLPSAEVALQA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 LYVFVGQDFRERLIHSLPTSLERALSEDSAPTNDTAANSASPPAETELQA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 RVLTAVVASFFICWFFFQLVALLGTVWLKEMLFYGKYKIIDILVNFTSSLAFFNSCLNEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 LDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIA
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                        amino acida
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVLSFVAAAFFLCWSFYQVVALIATVRIRELL-QGMYKEIGIAVDVTSALAFFNSCLNFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LDRCVCVLHPVWTQNHRTVSLAKKVIIGPWVMALLLTLPVIIRVTTVPGKTGTVACTFNF
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                                                                                                                                                                                                                                                                                                                                                                 Version #1.25
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: P
FRAGMENT TYPE: N
ORIGINAL SOURCE:
ORGANISM: Homo
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CLONE: F-PEP
300
                                                                                                                                181
                 301 LYVFVGQDFRERLIHSLPTSLERALSEDSAPTNDTAANSASPPAETELQA 350
                                                                241
                                                                                                                                                         181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPL 240
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                                                                                             241 RVLTAVVASFFICWFFFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPM 300
                                                                                                                                                                                                                   121 LDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNF 180
                                                                                                                                                                                                                                                                61 TISYLNLAVADECETSTLEEEMVRKAMGGHWEEGWELCKEVETIVDINLEGSVELIALIA 120
                                                                                                                                                                                                                                                                                  61 TICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIA 120
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                                                                                                                                SPWINDPKERIKVAVAMLTVRGIIRGIIGFSAPMSIVAVSYGLIATKIHKQGLIKSSRPL
                                                                                                                                                                                               LDRCVCVLHPVWTQNHRTVSLAKKVIIGPWVMALLLTLPVIIRVTTVPGKTGTVACTFNF
LYVFMGQDFRERLIHALPASLERALTEDSTQTSDTATNSTLPSAEVALQA 349
                                                             Conservative
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N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                             68.3%; Score 1240.5; 68.6%; Pred. No. 3.4e
                                                                                                                                                                                                                                                                                                                                                                                            37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               3.4e-84
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Length 350;
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                                                                  299
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US-08-458-970A-10 CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION UNMER: PCT/US94/09234

PILING DATE: 16 AUG 1994

ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-353
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 10: Patent No. 5861272
GENERAL INFORMATION: Sequence 10, COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOPTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/45;
FILING DATE: June 2, 1995 ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE TITLE OF INVENTION: C NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS: ADDRESSEE: STREET: 6 BECKI COUNTRY: NEW JERSEY Application US/08458970A E: CARELLA, BYRNE, BAIN, GILFILLAN
E: CECCHI, STEWART & OLSTEIN
6 BECKER FARM ROAD USA C5a Receptor US/08/458,970A 325800-353

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RESULT 7
US-08-118-270-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 34, Applicati
Patent No. 5508384
GENERAL INFORMATION:
                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION UMMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NUMBER: TENTORY EXPLORES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 64.6%; Score 1174.5; DB 1; Length 364; Best Local Similarity 64.6%; Pred. No. 2.7e-79; Matches 237; Conservative 38; Mismatches 73; Indels 19;
                                                                                                                                                                                                                                                               ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF
TITLE OF INVENTION: RECEPTORS, AND
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acid
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MU
                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                   STREET: 419 Sever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                    STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358 ENTLNAM 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPLAFFNSCLNPMLYVFMGQDFRERLIHSLPASLERALTEDSAQTSDTGTNLGTNSTSLS 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSLAFFNSCLNPMLYVFVGQDFRERLIHSLPTSLERALSEDSAPTNDTAAN----SASPPA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IHRQGLIKSSRPLRVLSFVVAAFFLCWCPFQVVALISTIQVRERLKNMTPGIVTAL-KIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ETELQAM 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08118270
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419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                     Floppy disk
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    MURPHY=2A
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ND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                               Suite 300
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PCT-US93-08528-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 34, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 248633
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acide
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                             ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                      APPLICATION NUMBER: PCT/US93/0852
FILING DATE: 09-SEP-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
                                                                 FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
TELECOMMUNICATION
                                                                                                                                                                                                                                                                                                       STREET:
CITY: Wa
STATE: D
COUNTRY:
              NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MU
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TELEFAX: 202-737-3528
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                                                                                                                                                                                                                                                                                                                                          Washington
                                                                                                                                                                                                                                                                                                                           D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVTTICYLNLALADFSFTATLPFLIVSMA 86
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                                                                                                                                                                                                                                                                                                           USA
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 INFORMATION
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                                                                                                                                                             PCT/US93/08528
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                MURPHY=2 PCT
                                                                                                                                                                                                  Version #1.25
                                                                                                                                                                                                                                                                                                                                                               Suite 300
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RESULT 9
US-08-513-974B-348
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Best Local Similarity 67.3%;
Matches 218; Conservative 3
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APPLICANT: Hinuma,
APPLICANT: HOSOYa,
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hosoya, Masaki
APPLICANT: Pujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Pukusumi, Shoji
APPLICANT: Pukusumi, Shoji
APPLICANT: Ohgi, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCES: 380
                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION WINBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
CLASSIFICATION: 536
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LENGTH: 315 amino acide
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ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                       STATE: N
COUNTRY:
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TELEFAX: 202-7
TELEX: 248633
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                                                                                                                                                                                                                                                                                                    130 Water Street
                                                                                                                                                                                                                                       USA
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      PCT/JP95/01599
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Pred. No. 4.1e-75;
7; Mismatches 59
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RESULT 10
US-09-170-496D-246
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US-08-513-974B-348
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Sequence 246, Application US/09170496D Patent No. 6555339
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endoge
                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
PILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
PILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION UNMEER: JP 6-236356
FILING DATE: 30-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 125 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: JP 6-326611 FILING DATE: 28-DEC-1994
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99.2%;
   6555339-Endogenous, Constitutively Activated Human G Protein-(
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Pred. No. 2.6e-39;
                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
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; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILLING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 246
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-170-496D-270
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                                                                                                                                                                                                                             TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 270
LENGTH: 356
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                             Matches
                                                                                                                                                             Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 270, Application US/09170496D Patent No. 6555339 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 30.5%; Score 554.5; DB 2
Best Local Similarity 41.0%; Pred. No. 1.5e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Behan, Dominic P. APPLICANT: Chalmers, Derek T. APPLICANT: Liaw, Chen W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -09-170-496D-246
                                                                                                                                                              Local Similarity
 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336 ARAFGEE 342
                                                                                                                                             126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322 ERALSED 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 LLVHLWRRVMLKEIYHPRMLLILQASFALGCVNSSLNPFLYVFVGRDFQEKFFQSLTSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 LLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPMLYVFVGQDFRERLIHSLPTSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 TIGHFLLGFLGPLAIIGTCAHLIRAKLLREGWVHANRPARLLLVLVSAFFIFWSPFNVV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202 GIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVLTAVVASFFICWFPFQLVA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 AMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNFASWGGTPBERLKVAITMLTAR 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 IVS----ROWLLGEWACKLYITEVELSYFASNCLLVFISVDRCISVLYFVWALNHRTVQR 157
                                                                      82 IVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRCICVLHPVWAQNHRTVSL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 IVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRCICVLHPVWAQNHRTVSL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 LRILPLVVLGVTFVLGVLGNGLVIWVAGFRWTRTVTTTCYLNLALADFSFTATLP---FL 81
IVS----RQWLLGEWACKLYITFVFLSYFASNCLLVFISVDRCISVLYPVWALNHRTVQR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASWLAPGVWLLAAALCSAHLKPRITRKW-NGCTHCYLAPNSDNETAQIWIEGVVEGHIIG
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                                                                                                                                            Conservative
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                                                                                                                                                             30.5%; Score 553.5; DB 2
                                                                                                                                            59; Mismatches 113;
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                                                                                                                                                                              DB 2;
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                                                                                                                                                                           Query Match 28.2%; Score 513; DB 1; I Best Local Similarity 33.6%; Pred. No. 1.8e-30; Matches 122; Conservative 60; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/08458970A Patent No. 5861272
                                                                                                                                                                                                                                                                                                                                                                                   TELEPAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/458

FILING DATE: JUNE 2, 1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/

FILING DATE: 16 AUG 1994

ATTORNEY/AGENT INFORMATION:

NAME: MULLINS, J.G.

REGISTRATION NUMBER: 33,073

REGISTRATION NUMBER: 33,073
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                                                                                                                                                                                                                                                                                             STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKE
COMPUTER: 1BM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336 ARAFGEE 342
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65
                                      54 RMTRTVTTICYLNLALADESETATLEELIVSMAMGEKWEEGWELCKLIHIVVDINLEGSV 113
EAKRTINAIWFLNLAVADFLSCLALPILFTSIVQHHHWPFGGAACSILPSLILLNMYASI
                                                                                                                                NFSTP-LNEYEB-----VSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAGF
                                                                                   NYTTPDYGHYDDKDTLDLNTPVDKTSNTLRVPDILALVIFAVVFLVGVLGNALVVWVTAF
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                                                                                                                                                                                                                                                                                                                                                                                          350 amino acids
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                                                                                                                                                                                                                           Length 350;
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                                                                                                                                                                                52;
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APPLICANT: Ye, Richard D
INTELE OF INVENTION: A G PROTEIN-COUPLED RECEPTOR WITH AN ENLARGED
ITITLE OF INVENTION: EXTRACELLULAR DOMAIN
FILE REFERENCE: SCR20418
CURRENT APPLICATION NUMBER: US/09/117,440
CURRENT FILING DATE: 1998-07-28
EARLIER APPLICATION NUMBER: PCT/US97/01736
EARLIER APPLICATION NUMBER: PCT/US97/01736
EARLIER APPLICATION NUMBER: 60/010,808
EARLIER FILING DATE: 1997-01-30
EARLIER FILING DATE: 1996-01-30
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver: 2.1
SOFTWARE: Patentin Ver: 2.1
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US-09-117-440-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 482
                                                                                                                                                            174
                                                                                                                                                                                                                                                                        118 FIALDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             342 TMA 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    335 TAA 337
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  294
                                         191 LKV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282 DSLCVSFAYINCCINPIIYVVAGQGFQGRLRKSLPSLLRNVLTEESVVRESKSFTRSTVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 TWSRRATRSTKTLKVVVAVVASFFIFWLPYQVTGIM-----MSFLEPSSPTFLLLNKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 FLIGFIALDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGD
                                                                                                                                                                                                                                                                                                                     55 TVNTIWFLHLTLADLLCCLSLPFSLAHLALQGQWPYGRFLCKLIPSIIVLNMFASVFLLT 114
                                                                                                                                                                                                                                                                                                                                                          58 TVTTICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIG 117
                                                                                                                                                                                                                                                                                                                                                                                                      7
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                                                                                                                                                                                                    FNFA-----
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                                                                                                                                                        YKFGLSSSLDYPDFYGDPLENRSLENIVQRPGEMNDRLDPSSFQTNDHPWTVPTVFQPQT
LKLFPSASSNSFYESELPQGFQDYYNLGQFTDDDQVPTPLVAITITRLVVGFLLPSVIMI 353
                                                                              FORPSADSLPRGSARLTSONLYSNVFKPADVVSPKIPSGFPIEDHETSPLDNSDAFLSTH
                                                                                                                                                                                                                                                                                                                                                                                                    ETNSTDLLSQPWNEPPV------ILSMVILSLTFLLGLPGNGLVLWVAGLKMQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.0%; Score 509.5; DB 2; Length 482; 26.6%; Pred. No. 4.4e-30; ative 59; Mismatches 117; Indels 193;
                                       ----AITMLTARGIIRFVIGFSLPMSIVA 218
                                                                                                                     ----GGTPEE-----R
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; Patent No.
; GENERAL IN
                                                                                                                                                                                                                                         TELEX: 846169
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 482 amino acids
TYPB: amino acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                         Matches
                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 23,031
REFERENCE/DOCKET NUMBER: P505
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 610-407-0700
TELEPHONE: 610-407-0701
TELEPAX: 610-407-0701
TELEX: 846160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 16-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 536
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bergima, Derk
APPLICANT: Foley, James
APPLICANT: Kumar, Chandrika
APPLICANT: Sarau, Henry
TITLE OF INVENTION: THERAPEUTIC AND SCREENING
TITLE OF INVENTION: METHODS USING C3A RECEPTOR AND C3A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 5
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CITY: VALLEY FORGE
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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TVNTIWFLHLTLADLLCCLSLPFSLAHLALQGQWPYGRFLCKLIPSIIVLNMFASVFLLT
                   TVTTICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIG 117
                                                                                        ETN----FSTPLNEYEEVSYESAGYTVLRILPLVVLGVTFVLGVLGVGLVIWVAGFRMTR 57
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                                                                      ETNSTDLLSQPWNEPPV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08876874
                                                                                                                                                                                                                                                                                                482 amino acids
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                                                                                                                                       28.0%; Score 508.5; DB 1; ilarity 26.6%; Pred. No. 5.2e-30; Conservative 59; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ames, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RATNER & PRESTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60/019,627
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                                                                                                                                         Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341
                                                                      ---ILSMVILSLTFLLGLPGNGLVLWVAGLKMQR
                                                                                                                                       Indels 193;
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                                                                                                                                       Gaps
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GENERAL IN CHRISTIAN LOW:

APPLICANT: Léhann-Bruinsma, Karin
APPLICANT: Léhann-Bruinsma, Karin
APPLICANT: Liaw, Chen W.

APPLICANT: Liaw, Chen W.

FITTLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
TITLE OF INVENTION: Protein-Coupled Receptors
FILE REFERENCE: AREN-207
CURRENT FILING DATE: 2001-04-05
FRIOR APPLICATION NUMBER: US/09/826,509
CURRENT FILING DATE: 2001-04-05
FRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 1908-10-13
NUMBER: PATENTION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: Patentin Version 2.1
SEQ ID NO 467
LENGTH: 350
TYPE: PRT
CORGANISM: Homo Sapiens
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US-09-826-509-467
; Sequence 467, Application
; Patent No. 6806054
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                          Query Match 27.9%; Score 507; DB 2; Length 350; Best Local Similarity 33.3%; Pred. No. 4.9e-30; Matches 121; Conservative 60; Mismatches 130; Indels
                         174
                                                                                                  114 FLIGFIALDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGD 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     397
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                                                                                                                                                                                     54 RMTRTVTTICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSV 113
                                                                                                                                                                                                                                                                      4
TY-----CTFNFASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAK 227
                                                               LLLATÍSADRFLLVFKPIWCÓNFRGAGLÁWIACAVAWGLÁLLLTIPSFLYRVV-----RE
                                                                                                                                            EAKRTINAIWFLNLAVADFLSCLALPILFTSIVQHHHWPFGGAACSILPSLILLNMYASI 124
                                                                                                                                                                                                                             NYTTPDYGHYDDKDTLDLNTPVDKTSNTLRVPDILALVIFAVVFLVGVLGNALVVWVTAF
                                                                                                                                                                                                                                                                      NESTP-LNEYEE-----VSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAGF 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIIDILVNPTS------SLAFFNSCLNPMLYVFVGQDFRERLIHSLPTSLER 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKLFPSASSNSFYESELFQGFQDYYNLGQFTDDDQVFTPLVAITITRLVVGFLLPSVIMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACYSFIVFRMQRGRFAKSQSKTFRVAVVVVAVFLVCWTPYHI-----F
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                         335 TAA 337
                                                   282 DSLCVSFAYINCCINPIIYVVAGQGFQGRLRKSLPSLLRNVLTEESVVRESKSFTRSTVD
                                                                              288
                                                                                                         229
                                                                                                                       180 EYFPPKVLCGVDYSH-----DKRRERAV-----AIVRLVLGFLWPLLTLTICYTFILLR
                                                                            SSL----AFFNSCLNPMLYVFVGQDFRERLIHSLPTSLERALSEDSA-----PTND 334
                                                                                                         TWSRRATRSTKTKKVVVAVVASPFIFWLPYQVTGIM-----MSFLEPSSPTFLLLNKL 281
TMA 344
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Search completed: March 28, 2006, 13:22:08
Job time: 63.712 secs